

OM protein - protein search, using sw model

Run on: September 29, 2004, 18:02:07 ; Search time 103.384 Seconds  
(without alignments)  
3219.466 Million cell updates/sec

Title: US-09-830-972-29  
Perfect score: 5923  
Sequence: 1 MEDLDQSPLVSSSDSPRPQ.....VKDAMAKIQAKIPGLKRKAE 1178

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_29Jan04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	5882	99.3	1178	3	AAY71311	Aay71311 Human neu
2	5815	98.2	1192	4	AAU04591	Aau04591 Human Nog
3	5815	98.2	1192	5	ABP68600	Abp68600 Human pan
4	5815	98.2	1192	6	ABR59667	Abr59667 Human Nog
5	5810	98.1	1192	3	AAY56967	Aay56967 Human MAG
6	5810	98.1	1192	4	AAB82349	Aab82349 Human NOG
7	5810	98.1	1192	5	ABG30938	Abg30938 Human Nog
8	5810	98.1	1192	5	ABB81078	Abb81078 Human neu
9	5526.5	93.3	1246	4	AAU33228	Aau33228 Novel hum

10	4560	77.0	983	6	ABU11573	Abu11573	Human MDD
11	4400	74.3	893	3	AAy95012	Aay95012	Human sec
12	4296.5	72.5	1163	3	AAy71310	Aay71310	Rat neuro
13	4296.5	72.5	1163	5	ABB81074	Abb81074	Rat neuro
14	4294.5	72.5	1162	3	AAy71557	Aay71557	Rat Nogo
15	4286.5	72.4	1163	3	AAy71384	Aay71384	Alternati
16	3388.5	57.2	974	3	AAy71560	Aay71560	Rat Nogo
17	3146.5	53.1	642	2	AAW58383	Aaw58383	Human sec
18	3146.5	53.1	642	4	AAB90682	Aab90682	Human BGl
19	2715	45.8	803	3	AAy71562	Aay71562	Rat Nogo
20	2529.5	42.7	737	3	AAy71386	Aay71386	Rat Nogo
21	2487.5	42.0	746	3	AAy71391	Aay71391	Rat Nogo
22	2457	41.5	736	3	AAy71398	Aay71398	Rat Nogo
23	2449.5	41.4	732	3	AAy71399	Aay71399	Rat Nogo
24	2405.5	40.6	695	3	AAy71387	Aay71387	Rat Nogo
25	2344.5	39.6	684	3	AAy71394	Aay71394	Rat Nogo
26	1948.5	32.9	552	3	AAy71388	Aay71388	Rat Nogo
27	1743	29.4	502	3	AAy71396	Aay71396	Rat Nogo
28	1634.5	27.6	475	3	AAy71389	Aay71389	Rat Nogo
29	1566.5	26.4	403	3	AAy71563	Aay71563	Rat Nogo
30	1552.5	26.2	457	3	AAy71392	Aay71392	Rat Nogo
31	1495.5	25.2	373	3	AAy53624	Aay53624	A bone ma
32	1495.5	25.2	373	3	AAy56969	Aay56969	Human MAG
33	1495.5	25.2	373	3	AAB24242	Aab24242	Human Nog
34	1495.5	25.2	373	4	AAB82350	Aab82350	Human NOG
35	1495.5	25.2	373	5	AAM47954	Aam47954	Human RTN
36	1495.5	25.2	373	5	ABP68601	Abp68601	Human pan
37	1495.5	25.2	373	5	ABB81079	Abb81079	Human neu
38	1487.5	25.1	373	5	ABG30937	Abg30937	Human Nog
39	1412	23.8	289	3	AAy56968	Aay56968	Human MAG
40	1327	22.4	284	3	AAy95030	Aay95030	Human clo
41	1264	21.3	356	3	AAy71390	Aay71390	Rat Nogo
42	1225.5	20.7	379	7	ADB85283	Adb85283	Rat fooce
43	1205.5	20.4	374	3	AAy71397	Aay71397	Rat Nogo
44	1196.5	20.2	361	3	AAy71385	Aay71385	Alternati
45	1189	20.1	359	3	AAy71558	Aay71558	Rat Nogo

# ALIGNMENTS

## RESULT 1

AAy71311

ID AAY71311 standard; protein; 1178 AA.

XX

AC AAY71311;

XX

DT 02-NOV-2000 (first entry)

XX

DE Human neurite growth inhibitor Nogo.

XX

KW Human; neurite growth inhibitor; Nogo; neural cell; myelin; CNS;

KW central nervous system; neoplastic disease; antiproliferative; glioma;

KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;

KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;

KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;

KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;

KW structural plasticity; screening.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT Misc-difference 187  
FT /label= Unknown  
FT Misc-difference 188  
FT /label= Unknown  
FT Misc-difference 189  
FT /label= Unknown  
FT Misc-difference 190  
FT /label= Unknown  
FT Misc-difference 221  
FT /label= Unknown  
FT Misc-difference 328  
FT /label= Unknown  
FT Misc-difference 477  
FT /label= Unknown  
FT Region 977. .1012  
FT /note= "Region specifically described in claim 16"  
FT Region 994. .1174  
FT /note= "Region specifically described in claim 16"  
FT Region 1079. .1114  
FT /note= "Region specifically described in claim 16"  
XX  
PN WO200031235-A2.  
XX  
PD 02-JUN-2000.  
XX  
PF 05-NOV-1999; 99WO-US026160.  
XX  
PR 06-NOV-1998; 98US-0107446P.  
XX  
PA (SCHW/) SCHWAB M E.  
PA (CHEN/) CHEN M S.  
XX  
PI Schwab ME, Chen MS;  
XX  
DR WPI; 2000-400052/34.  
XX  
PT Nogo proteins and nucleic acids useful for treating neoplastic disorders  
PT of the central nervous system and inducing regeneration of neurons.  
XX  
PS Claim 11; Fig 13; 122pp; English.  
XX  
CC The present sequence is a human Nogo protein which is a potent neural  
CC cell growth inhibitor and is free of all central nervous system (CNS)  
CC myelin material with which it is natively associated. The human Nogo  
CC sequence was derived by aligning human expressed sequence tags (ESTs)  
CC e.g. AA158636, AA333267, AA081783, AA167765, AA322918, AA092565, AA081525  
CC and AA081840 with the rat Nogo sequence. Nogo proteins and fragments  
CC displaying neurite growth inhibitory activity are used in the treatment  
CC of neoplastic disease of the CNS e.g. glioma, glioblastoma,  
CC medulloblastoma, craniopharyngioma, ependyoma, pinealoma,  
CC haemangioblastoma, acoustic neuroma, oligodendroglioma, menangioma,  
CC neuroblastoma or retinoblastoma and degenerative nerve diseases e.g.

CC Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo  
CC activity can be used to treat or prevent hyperproliferative or benign  
CC dysproliferative disorders e.g. psoriasis and tissue hypertrophy.  
CC Ribozymes or antisense Nogo nucleic acids can be used to inhibit  
CC production of Nogo protein to induce regeneration of neurons or to  
CC promote structural plasticity of the CNS in disorders where neurite  
CC growth, regeneration or maintenance are deficient or desired. The animal  
CC models can be used in diagnostic and screening methods for predisposition  
CC to disorders and to screen for or test molecules which can treat or  
CC prevent disorders or diseases of the CNS. Note: SEQ ID numbers 35-42 are  
CC referred in claim 32 and SEQ ID NO: 29 in disclosure of the  
CC specification. However the specification does not include sequences for  
CC these SEQ ID numbers

XX

SQ Sequence 1178 AA;

Query Match 99.3%; Score 5882; DB 3; Length 1178;  
Best Local Similarity 99.7%; Pred. No. 5.4e-296;  
Matches 1175; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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Qy      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEDEDEDLEELEVLERKPA 60
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Db      1 MEDLDQSPLVSSSDSVPRPQPAFKYQFVREPEDEEEEEEEEDEDEDLEELEVLERKPA 60

Qy     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSVTPAP 120
          |||
Db     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSVTPAP 120

Qy    121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPAPAPAAPSTPAAPKRRG 180
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Db    121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPAPAPAAPSTPAAPKRRG 180

Qy    181 SSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAASFKEHEYLGN 240
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Db    181 SSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAASFKEHEYLGN 240

Qy    241 LSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSVSPKAESAV 300
          |||
Db    241 LSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSVSPKAESAV 300

Qy    301 IVANPREEIIVKNKDEEEKLVSNILHXQQELPTALTCLVKEDEVVSSEKAKDSFNEKRV 360
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Db    301 IVANPREEIIVKNKDEEEKLVSNILHXQQELPTALTCLVKEDEVVSSEKAKDSFNEKRV 360

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Qy    421 EKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSENXTDE 480
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Qy    541 VQEACESELNEVTGTKIAYETKMDLVQTSSEVMQESLYPAAQLCPSFEESEATPSPVLPDI 600
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Qy	601	VMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSGIKE	660
Db	601	VMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSGIKE	660
Qy	661	EIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELV	720
Db	661	EIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELV	720
Qy	721	EDSSPDSEPVDLFSDDSIDVPQKQDETVMVLKESLTETSFESMIEYENKEKLSALPPEG	780
Db	721	EDSSPDSEPVDLFSDDSIDVPQKQDETVMVLKESLTETSFESMIEYENKEKLSALPPEG	780
Qy	781	GKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFISKEAQIRE	840
Db	781	GKPYLESFKLSLVNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFISKEAQIRE	840
Qy	841	TETFSDSPIEIIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTEL	900
Db	841	TETFSDSPIEIIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTEL	900
Qy	901	PHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPDVSALGHTQAEIESIVKPKVLE	960
Db	901	PHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPDVSALGHTQAEIESIVKPKVLE	960
Qy	961	KEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVF	1020
Db	961	KEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVF	1020
Qy	1021	SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS	1080
Db	1021	SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS	1080
Qy	1081	ALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI	1140
Db	1081	ALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI	1140
Qy	1141	YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1178
Db	1141	YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1178

# RESULT 2

AAU04591

ID AAU04591 standard; protein; 1192 AA.

XX

AC AAU04591;

XX

DT 26-SEP-2001 (first entry)

XX

DE Human Nogo protein.

XX

KW Human; Nogo receptor; axonal growth; immunogen; antibody; nogo protein;

KW cranial trauma; cerebral trauma; spinal cord injury; stroke;

KW demyelinating disease; multiple sclerosis; monophasis demyelination;

KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis;  
 KW Marchiafava-Bignami disease; pontine myelinolysis; adrenoleukodystrophy;  
 KW Pelizaeus-Merzbacher disease; Spongy degeneration; Alexander's disease;  
 KW Canavan's disease; metachromatic leukodystrophy; viral infection;  
 KW Krabbe's disease.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT Domain 1054. .1119  
 FT /label= Lumenal\_extracellular\_domain  
 FT /note= "This sequence is specifically claimed"  
 FT Peptide 1055. .1094  
 FT /label= Pep1  
 FT /note= "Receptor binding inhibitory peptide. This  
 FT sequence is specifically claimed"  
 FT Peptide 1064. .1088  
 FT /label= Pep2  
 FT /note= "Receptor binding inhibitory peptide. This  
 FT sequence is specifically claimed"  
 FT Peptide 1074. .1098  
 FT /label= Pep3  
 FT /note= "Receptor binding inhibitory peptide. This  
 FT sequence is specifically claimed"  
 FT Peptide 1084. .1108  
 FT /label= Pep4  
 FT /note= "Receptor binding inhibitory peptide. This  
 FT sequence is specifically claimed"  
 FT Peptide 1095. .1119  
 FT /label= Pep5  
 FT /note= "Receptor binding inhibitory peptide. This  
 FT sequence is specifically claimed"  
 XX  
 PN WO200151520-A2.  
 XX  
 PD 19-JUL-2001.  
 XX  
 PF 12-JAN-2001; 2001WO-US001041.  
 XX  
 PR 12-JAN-2000; 2000US-0175707P.  
 PR 26-MAY-2000; 2000US-0207366P.  
 PR 29-SEP-2000; 2000US-0236378P.  
 XX  
 PA (UYYA ) UNIV YALE.  
 XX  
 PI Strittmatter SM;  
 XX  
 DR WPI; 2001-442138/47.  
 DR N-PSDB; AAS09453.  
 XX  
 PT Novel Nogo receptor protein useful for identifying modulator of Nogo  
 PT protein or Nogo receptor protein, which is useful for treating central  
 PT nervous system disorders.  
 XX  
 PS Example 1; Page 101-104; 109pp; English.  
 XX  
 CC The sequence is the human Nogo protein, a 250kDa myelin-associated axon

CC growth inhibitor. The invention relates to the use of the nogo receptor,  
CC nogo protein, their nucleic acids, vectors expressing them and antibodies  
CC against them, to isolate agents which block nogo receptor mediated axonal  
CC growth. The agent is useful for treating a central nervous system  
CC disorder which is a result of cranial or cerebral trauma, spinal cord  
CC injury, stroke or a demyelinating disease selected from multiple  
CC sclerosis, monophasis demyelination, encephalomyelitis, multifocal  
CC leukoencephalopathy, panencephalitis, Marchiafava-Bignami disease,  
CC pontine myelinolysis, adrenoleukodystrophy, Pelizaeus-Merzbacher disease,  
CC Spongy degeneration, Alexander's disease, Canavan's disease,  
CC metachromatic leukodystrophy, viral infection and Krabbe's disease

XX

SQ Sequence 1192 AA;

Query Match 98.2%; Score 5815; DB 4; Length 1192;  
Best Local Similarity 97.2%; Pred. No. 1.6e-292;  
Matches 1160; Conservative 4; Mismatches 13; Indels 16; Gaps 3;

Qy	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Db	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVVSSTVPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVVSSTVPAP	120
Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Qy	181	SSGA-----VXXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSLSP	226
		: : :	
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSLSP	240
Qy	227	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	286
Db	241	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	287	GSSFVSVPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTCLVKEDEVV	346
Db	301	GSSFVSVPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHNQQELPTALTCLVKEDEVV	360
Qy	347	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	406
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	407	DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	466
Db	421	DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	480
Qy	467	PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTQVTE	526
Db	481	PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTQVTE	540
Qy	527	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	586
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600

Qy	587	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	646
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	647	EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSE	705
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSE	720
Qy	706	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFESMI	765
Db	721	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFESMI	780
Qy	766	EYENKEKLSALPPEGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	825
Db	781	EYENKEKLSALPPEGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	826	SNDDLFIKSEAQIRETETFSDDSSPIEIIIDFPTLISSKTDSFSKLAREYTDLEVSHKSEI	885
Db	841	SNDDLFIKSEAQIRETETFSDDSSPIEIIIDFPTLISSKTDSFSKLAREYTDLEVSHKSEI	900
Qy	886	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSA LGH	945
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSA LA-	959
Qy	946	TQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSA DLGKTSVVDLLYWRDIKKTGV	1005
Db	960	TQAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSA ELSKTSVVDLLYWRDIKKTGV	1019
Qy	1006	VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES	1065
Db	1020	VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES	1079
Qy	1066	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT	1125
Db	1080	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT	1139
Qy	1126	LLILALISLFSVPVIYERHQAQIDHYLG LANKNVKDAMAKIQAKIPGLKRKAE	1178
Db	1140	LLILALISLFSVPVIYERHQAQIDHYLG LANKNVKDAMAKIQAKIPGLKRKAE	1192

RESULT 3

ABP68600

ID ABP68600 standard; protein; 1192 AA.

XX

AC ABP68600;

XX

DT 14-JAN-2003 (first entry)

XX

DE Human pancreatic cancer expressed protein SEQ ID NO 71.

XX

KW Human; pancreas; cancer; gene therapy; vaccine; immunostimulant;  
cytostatic; tumour.

XX

OS Homo sapiens.

XX

PN WO200260317-A2.  
 XX  
 PD 08-AUG-2002.  
 XX  
 PF 30-JAN-2002; 2002WO-US002781.  
 XX  
 PR 30-JAN-2001; 2001US-0265305P.  
 PR 31-JAN-2001; 2001US-0265682P.  
 PR 09-FEB-2001; 2001US-0267568P.  
 PR 21-MAR-2001; 2001US-0278651P.  
 PR 28-APR-2001; 2001US-0287112P.  
 PR 16-MAY-2001; 2001US-0291631P.  
 PR 12-JUL-2001; 2001US-0305484P.  
 PR 20-AUG-2001; 2001US-0313999P.  
 PR 27-NOV-2001; 2001US-0333626P.  
 XX  
 PA (CORI-) CORIXA CORP.  
 XX  
 PI Benson DR, Kalos MD, Lodes MJ, Persing DH, Hepler WT, Jiang Y;  
 XX  
 DR WPI; 2002-627435/67.  
 DR N-PSDB; ABV94680.  
 XX  
 PT New isolated polynucleotide and pancreatic tumor polypeptides, useful for  
 PT diagnosing, preventing and/or treating cancer, particularly pancreatic  
 PT cancer.  
 XX  
 PS Claim 2; SEQ ID NO 71; 300pp + Sequence Listing; English.  
 XX  
 CC The invention relates to an isolated polynucleotide (I) comprising: (a)  
 CC any of a group of over 4000 nucleotide sequences (ABV94628-ABV99145); (b)  
 CC complements of (a); (c) sequences consisting of at least 20 contiguous  
 CC residues of (a); (d) sequences that hybridize to (a), under moderately  
 CC stringent conditions; (e) sequences having at least 75% or 90% identity  
 CC to (a); or (f) degenerate variants of (a). Polypeptides (ABP68596-  
 CC ABP68637) encoded by (I) and oligonucleotide can be used to detect cancer  
 CC in a patient and compositions comprising polypeptides, polynucleotides,  
 CC antibodies, fusion proteins, T cell populations and antigen presenting  
 CC cells expressing the polypeptide are useful in treating pancreatic cancer  
 CC and stimulating an immune response. The polynucleotides can be used as  
 CC probes or primers for nucleic acid hybridisation, in the design and  
 CC preparation of ribozyme molecules for inhibiting expression of the tumour  
 CC polypeptides and proteins in the tumour cells, in vaccines and for gene  
 CC therapy. Note: The sequence data for this patent did not form part of the  
 CC printed specification, but was obtained in electronic format directly  
 CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 1192 AA;

Query Match 98.2%; Score 5815; DB 5; Length 1192;  
 Best Local Similarity 97.2%; Pred. No. 1.6e-292;  
 Matches 1160; Conservative 4; Mismatches 13; Indels 16; Gaps 3;

Qy 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEDEDEDLEELEVLERKPA 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEDEDEDLEELEVLERKPA 60

Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVPSSTVPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVPSSTVPAP	120
Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Qy	181	SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP	226
		:  : :	
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP	240
Qy	227	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	286
Db	241	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	287	GSSFSVSPKAESAVIVANPREEIIIVKNKDEEEKLVSNILHXQQELPTALTCLKVKEDEVV	346
Db	301	GSSFSVSPKAESAVIVANPREEIIIVKNKDEEEKLVSNILHNQQELPTALTCLKVKEDEVV	360
Qy	347	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	406
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	407	DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	466
Db	421	DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	480
Qy	467	PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTE	526
Db	481	PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTE	540
Qy	527	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	586
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	587	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	646
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	647	EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFS DYSE	705
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFS DYSE	720
Qy	706	MAKVEQPVPDHSSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETS FESMI	765
Db	721	MAKVEQPVPDHSSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETS FESMI	780
Qy	766	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	825
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	826	SNDDLFI SKEAQIRETETFS DSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI	885
Db	841	SNDDLFI SKEAQIRETETFS DSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI	900
Qy	886	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFS KN GSATS K VLLL PPDVSALGH	945

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          |||
Db      901 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLLPPDVSALA- 959
Qy      946 TQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGV 1005
          |||
Db      960 TQAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGV 1019
Qy      1006 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES 1065
          |||
Db      1020 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES 1079
Qy      1066 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT 1125
          |||
Db      1080 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT 1139
Qy      1126 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
          |||
Db      1140 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192

```

RESULT 4

ABR59667

ID ABR59667 standard; protein; 1192 AA.

XX

AC ABR59667;

XX

DT 22-JUL-2003 (first entry)

XX

DE Human NogoA protein.

XX

KW Human; Nogo receptor; NgR; CTS domain; neuroprotective; gene therapy;  
 KW axonal growth; central nervous system; CNS; Nogo; spinal cord injury;  
 KW cranial trauma; cerebral trauma; spinal trauma; stroke; Krabbe's disease;  
 KW demyelinating disease; multiple sclerosis; monophasic demyelination;  
 KW encephalomyelitis; multifocal leukoencephalopathy; panencephalitis.

XX

OS Homo sapiens.

XX

PN WO2003031462-A2.

XX

PD 17-APR-2003.

XX

PF 04-OCT-2002; 2002WO-US032007.

XX

PR 06-OCT-2001; 2001US-00972599.

XX

PA (UYYA ) UNIV YALE.

XX

PI Strittmatter SM;

XX

DR WPI; 2003-393433/37.

DR N-PSDB; ACC81048.

XX

PT New human Nogo receptor polypeptides and nucleic acids, useful for  
 PT decreasing inhibition of axonal growth by a central nervous system  
 PT neuron, or in treating central nervous system disease, disorder or  
 PT injury, e.g. spinal cord injury.





Db	421	DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	480
Qy	467	PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTQVTE	526
Db	481	PLLDGPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTQVTE	540
Qy	527	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	586
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	587	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	646
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	647	EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFS DYSE	705
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFS DYSE	720
Qy	706	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETS FESMI	765
Db	721	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETS FESMI	780
Qy	766	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	825
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	826	SNDDLFI SKEAQIRETETFS DSSPIEII DEFPTLISSKTDSFSKLAREYTDLEVSHKSEI	885
Db	841	SNDDLFI SKEAQIRETETFS DSSPIEII DEFPTLISSKTDSFSKLAREYTDLEVSHKSEI	900
Qy	886	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFS KN GSATSKVLLLPPDV SALGH	945
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFS KN GSATSKVLLLPPDV SALA-	959
Qy	946	TQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIF SADLGKTSVVDLLYWRDIKKTGV	1005
Db	960	TQAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGV	1019
Qy	1006	VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES	1065
Db	1020	VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES	1079
Qy	1066	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT	1125
Db	1080	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT	1139
Qy	1126	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1178
Db	1140	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1192

RESULT 5

AA56967

ID AAY56967 standard; protein; 1192 AA.

XX

AC AAY56967;

XX  
 DT 25-APR-2000 (first entry)  
 XX  
 DE Human MAGI polypeptide.  
 XX  
 KW MAGI protein; neuroendocrine-specific protein; neuropathy; human;  
 KW spinal injury; neuronal degeneration; neuromuscular disorder; cancer;  
 KW psychiatric disorder; developmental disorder; inflammatory disorder;  
 KW stroke; cytostatic; cerebroprotective; neuroprotective.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200005364-A1.  
 XX  
 PD 03-FEB-2000.  
 XX  
 PF 21-JUL-1999; 99WO-GB002360.  
 XX  
 PR 22-JUL-1998; 98GB-00016024.  
 PR 19-JUL-1999; 99GB-00016898.  
 XX  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX  
 PI Michalovich D, Prinjha RK;  
 XX  
 DR WPI; 2000-182693/16.  
 DR N-PSDB; AAZ56886.  
 XX  
 PT Novel polypeptides related to neuroendocrine-specific proteins and  
 PT polynucleotides useful for diagnosis of various diseases and for  
 PT treatment of cancer and neurological disorders.  
 XX  
 PS Claim 2; Page 20-21; 35pp; English.  
 XX  
 CC The invention relates to human MAGI protein, which is similar to  
 CC neuroendocrine-specific protein. The MAGI protein can be expressed by  
 CC standard recombinant methodology. The MAGI polypeptides, polynucleotides  
 CC and antibodies are useful for treating diseases, including neuropathies,  
 CC spinal injury, neuronal degeneration, neuromuscular disorders,  
 CC psychiatric disorders and developmental disorders, cancer, stroke and  
 CC inflammatory disorders. The polynucleoitde is also useful for chromosome  
 CC localization and for tissue expression studies. The present sequence  
 CC represents the human MAGI protein  
 XX  
 SQ Sequence 1192 AA;

Query Match 98.1%; Score 5810; DB 3; Length 1192;  
 Best Local Similarity 97.2%; Pred. No. 2.9e-292;  
 Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;

Qy	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPED	EEEEEEEEEEEEDEDEDLEELEVL	KPA	60
Db	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPED	EEEEEEEEEEEEDEDEDLEELEVL	KPA	60
Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWD	PSVSS	TVPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWD	PSVSS	TVPAP	120

Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Qy	181	SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP	226
		:   :	
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP	240
Qy	227	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	286
Db	241	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	287	GSSFSVSPKAESAVIVANPREEIIIVKNKDEEEKLVSNILHXQQELPTALTCLKVEDEVV	346
Db	301	GSSFSVSPKAESAVIVANPREEIIIVKNKDEEEKLVSNILHNQQELPTALTCLKVEDEVV	360
Qy	347	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	406
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	407	DKKCFADSLEQTNHEKDSSESNDDTSFSPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	466
Db	421	DKKCFADSLEQTNHEKDSSESNDDTSFSPSTPEGIKDRPGAYITCAPFNPAATESIATNIF	480
Qy	467	PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTE	526
Db	481	PLLGDPPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE	540
Qy	527	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	586
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	587	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	646
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	647	EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSE	705
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSE	720
Qy	706	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETSFESMI	765
Db	721	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETSFESMI	780
Qy	766	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	825
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	826	SNDDLFI SKEAQIRETETFS DSSPIEIIDEFPTLISSKTD SFSKLAREYTDLEVSHKSEI	885
Db	841	SNDDLFI SKEAQIRETETFS DSSPIEIIDEFPTLISSKTD SFSKLAREYTDLEVSHKSEI	900
Qy	886	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATS KVL LPPDV SALGH	945
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATS KVL LPPDV SALA-	959

Qy 946 TQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGV 1005  
 |||:|  
 Db 960 TQAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFS AELSKTSVVDLLYWRDIKKTGV 1019

Qy 1006 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLES 1065  
 |||  
 Db 1020 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIQAIQKSDEGHPFRAYLES 1079

Qy 1066 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLKLFAVLMWVFTYVGALFNGLT 1125  
 |||  
 Db 1080 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLKLFAVLMWVFTYVGALFNGLT 1139

Qy 1126 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178  
 |||  
 Db 1140 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192

RESULT 6

AAB82349

ID AAB82349 standard; protein; 1192 AA.

XX

AC AAB82349;

XX

DT 23-JUL-2001 (first entry)

XX

DE Human NOGO-A protein.

XX

KW NOGO-A; human; chromosome 2p21; neuropathy; spinal injury; brain injury;  
 KW stroke; neuronal degeneration; Alzheimer's disease; Parkinson's disease;  
 KW neuromuscular disorder; psychiatric disorder; developmental disorder;  
 KW neuroprotective; nootropic; neuroleptic; antiparkinsonian;  
 KW cerebroprotective; neuroleptic; diagnosis; therapy.

XX

OS Homo sapiens.

XX

PN WO200136631-A1.

XX

PD 25-MAY-2001.

XX

PF 14-NOV-2000; 2000WO-GB004345.

XX

PR 15-NOV-1999; 99GB-00026995.

PR 24-JAN-2000; 2000GB-00001550.

XX

PA (SMIK ) SMITHKLINE BEECHAM PLC.

XX

PI Michalovich D, Prinjha R;

XX

DR WPI; 2001-343822/36.

DR N-PSDB; AAF90324.

XX

PT New polypeptide designated NOGO-C is a splice variant of the human NOGO  
 PT gene and may be useful in the treatment of neural disorders including  
 PT Alzheimer's and Parkinson's diseases.

XX

PS Disclosure; Page 26-27; 25pp; English.

XX



Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	587	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	646
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	647	EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE	705
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE	720
Qy	706	MAKVEQPVPDHSSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFESMI	765
Db	721	MAKVEQPVPDHSSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFESMI	780
Qy	766	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	825
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	826	SNDDLFIKSEAQIRETETFSDDSSPIEIIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI	885
Db	841	SNDDLFIKSEAQIRETETFSDDSSPIEIIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI	900
Qy	886	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDV SALGH	945
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDV SALA-	959
Qy	946	TQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGV	1005
Db	960	TQAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFS AELSKTSVVDLLYWRDIKKTGV	1019
Qy	1006	VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES	1065
Db	1020	VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES	1079
Qy	1066	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFITYVGALFNGLT	1125
Db	1080	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFITYVGALFNGLT	1139
Qy	1126	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1178
Db	1140	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1192

RESULT 7

ABG30938

ID ABG30938 standard; protein; 1192 AA.

XX

AC ABG30938;

XX

DT 21-OCT-2002 (first entry)

XX

DE Human NogoA protein.

XX

KW Human; Nogo; BACE; acute neuronal injury; spinal injury; head injury;  
 KW stroke; peripheral nerve damage; neoplastic disorder; glioblastoma;  
 KW neuroblastoma; hyperproliferative disorder; dysproliferative disorder;

KW cirrhosis; psoriasis; keloid formation; fibrocystic condition; cancer;  
 KW tissue hypertrophy; central nervous system; axon regeneration; NogoA;  
 KW Nogo-associated disease; metastasis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200257483-A2.  
 XX  
 PD 25-JUL-2002.  
 XX  
 PF 18-JAN-2002; 2002WO-GB000228.  
 XX  
 PR 18-JAN-2001; 2001GB-00001312.  
 XX  
 PA (GLAX ) GLAXO GROUP LTD.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 XX  
 PI Blackstock WP, Hale RS, Prinjha R, Rowley A;  
 XX  
 DR WPI; 2002-599722/64.  
 DR N-PSDB; ABK90134.  
 XX  
 PT Identifying modulators of Nogo or BACE activity for treating acute  
 PT neuronal injuries, neoplastic or dysproliferative disorders, comprises  
 PT providing and monitoring interaction between Nogo and BACE polypeptides.  
 XX  
 PS Disclosure; Page 59-62; 68pp; English.  
 XX  
 CC The present invention relates to a new method of identifying modulators  
 CC of Nogo function or BACE activity. The method involves providing Nogo and  
 CC BACE polypeptides capable of binding with each other, monitoring the  
 CC interaction between these polypeptides, and determining if the test agent  
 CC is a modulator of Nogo or BACE activity. The method is useful in treating  
 CC acute neuronal injuries, such as spinal or head injury, stroke,  
 CC peripheral nerve damage, and in neoplastic (e.g. glioblastomas,  
 CC neuroblastomas), hyperproliferative or dysproliferative disorders (e.g.  
 CC cirrhosis, psoriasis, keloid formation, fibrocystic conditions, tissue  
 CC hypertrophy) of the central nervous system. The BACE polypeptide is  
 CC useful in screening methods to identify agents that may act as modulators  
 CC of BACE activity and in particular agents that may be useful in treating  
 CC Nogo-associated diseases. The modulators of Nogo or BACE polypeptides,  
 CC and the polynucleotide encoding the BACE polypeptide are useful in  
 CC manufacturing a medicament for the treatment or prevention of disorders  
 CC responsive to the modulation of Nogo activity, in alleviating the  
 CC symptoms or improving the condition of a patient suffering from this  
 CC disorder, in axon regeneration, or in preventing metastasis or spreading  
 CC of a cancer. The polynucleotide may also be an essential component in  
 CC assays, a probe, in recombinant protein synthesis, and in gene therapy  
 CC techniques. The present amino acid sequence represents the human NogoA  
 CC protein of the invention  
 XX  
 SQ Sequence 1192 AA;

Query Match 98.1%; Score 5810; DB 5; Length 1192;  
 Best Local Similarity 97.2%; Pred. No. 2.9e-292;  
 Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;

Qy	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Db	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVPSSTVPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVPSSTVPAP	120
Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Qy	181	SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP	226
		:   :	
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP	240
Qy	227	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	286
Db	241	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	287	GSSFVSVPKAESAVIVANPREEIIIVKNKDEEEKLVSNNILHXQQELPTALTCLVKEDEVV	346
Db	301	GSSFVSVPKAESAVIVANPREEIIIVKNKDEEEKLVSNNILHNQQELPTALTCLVKEDEVV	360
Qy	347	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	406
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	407	DKKCFADSLEQTNHEKDSSESSNDDTSFSPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	466
Db	421	DKKCFADSLEQTNHEKDSSESSNDDTSFSPSTPEGIKDRPGAYITCAPFNPAATESIATNIF	480
Qy	467	PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTE	526
Db	481	PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE	540
Qy	527	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	586
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	587	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE	646
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	647	EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSE	705
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSE	720
Qy	706	MAKVEQPVPDHSSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFESMI	765
Db	721	MAKVEQPVPDHSSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFESMI	780
Qy	766	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	825
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	826	SNDDLFIKSEAQIRETETFSDDSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI	885



Db	841	SNDDLFI SKEAQIRETETFS DSSPIEIIDEFPTLISSKTD SFSKLAREYTDLEVSHKSEI	900
Qy	886	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATS KVL LPPDV SALGH	945
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATS KVL LPPDV SALA-	959
Qy	946	TQAEIESIVKPKVLEKEAEKKLPSTEKEDRSPSAIF SADLGKTSVVDLLYWRDIKKTGV	1005
Db	960	TQAEIESIVKPKVLVKEAEKKLPSTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGV	1019
Qy	1006	VFGASLFL LLSLT VFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRAYLES	1065
Db	1020	VFGASLFL LLSLT VFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRAYLES	1079
Qy	1066	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT	1125
Db	1080	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT	1139
Qy	1126	LLILALISLFSVPVIYERHQAQIDHYLG LANKNVKDAMAKIQAKIPGLKRKAE	1178
Db	1140	LLILALISLFSVPVIYERHQAQIDHYLG LANKNVKDAMAKIQAKIPGLKRKAE	1192

RESULT 8

ABB81078

ID ABB81078 standard; protein; 1192 AA.

XX

AC ABB81078;

XX

DT 05-NOV-2002 (first entry)

XX

DE Human neurotransmitter receptor protein Nogo-A.

XX

KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;  
 KW central nervous system; peripheral nervous system; tranquillizer; Nogo;  
 KW vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;  
 KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;  
 KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;  
 KW neurotransmitter receptor; human; receptor.

XX

OS Homo sapiens.

XX

PN US2002072493-A1.

XX

PD 13-JUN-2002.

XX

PF 28-JUN-2001; 2001US-00893348.

XX

PR 19-MAY-1998; 98IL-00124500.

PR 21-JUL-1998; 98WO-US014715.

PR 22-DEC-1998; 98US-00218277.

PR 19-MAY-1999; 99US-00314161.

XX

PA (YEDA ) YEDA RES & DEV CO LTD.

XX

PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;

PI Moalem G;  
 XX  
 DR WPI; 2002-607255/65.  
 DR N-PSDB; ABN86601.  
 XX  
 PT Promoting nerve regeneration and preventing neuronal degeneration in the  
 PT central/peripheral nervous system from injury/disease, comprises  
 PT administering nervous system-specific activated T cells/antigen, or  
 PT analogs/peptides.  
 XX  
 PS Example; Page 53-56; 93pp; English.  
 XX  
 CC The invention relates to promoting nerve regeneration or conferring  
 CC neuroprotection and preventing or inhibiting neuronal degeneration in the  
 CC central/peripheral nervous system (NS). The method involves administering  
 CC NS-specific activated T cells, NS-specific antigen, its analogue or its  
 CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or  
 CC combinations. The method is useful for promoting nerve regeneration and  
 CC preventing neuronal degeneration in central/peripheral nervous system  
 CC from injury/disease, where the injury is spinal cord injury, blunt  
 CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or  
 CC damages caused by surgery such as tumour excision. The disease is not an  
 CC autoimmune disease or neoplasm. The disease results in a degenerative  
 CC process occurring in either gray or white matter or both. The disease is  
 CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's  
 CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,  
 CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and  
 CC vitamin deficiency, intervertebral disc herniation, prion diseases such  
 CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral  
 CC neuropathies associated with various diseases, including but not limited  
 CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute  
 CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary  
 CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption  
 CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-  
 CC pathies, complications of various drugs (e.g., metronidazole) and toxins  
 CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia  
 CC telangectasia, Friedreich's ataxia, amyloid polyneuropathies,  
 CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's  
 CC disease, or lipoproteinemia. The present sequence represents the human  
 CC neurotransmitter receptor protein Nogo-A, an example of NS-specific  
 CC antigen  
 XX  
 SQ Sequence 1192 AA;

Query Match 98.1%; Score 5810; DB 5; Length 1192;  
 Best Local Similarity 97.2%; Pred. No. 2.9e-292;  
 Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;

Qy	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Db	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSFVSSTVPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSFVSSTVPAP	120
Qy	121	SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKRRG	180

Db	121	SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVWTFPAPAPAAPSTPAAPKRRG	180
Qy	181	SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP	226
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP	240
Qy	227	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	286
Db	241	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	287	GSSFVSVPKAESAVIVANPREEIIVKNKDEEEKLVSNILHXQQELPTALTCLKVKEDEVV	346
Db	301	GSSFVSVPKAESAVIVANPREEIIVKNKDEEEKLVSNILHNQQELPTALTCLKVKEDEVV	360
Qy	347	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	406
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	407	DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	466
Db	421	DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF	480
Qy	467	PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTE	526
Db	481	PLLGDPPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE	540
Qy	527	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	586
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	587	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	646
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	647	EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE	705
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE	720
Qy	706	MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETS FESMI	765
Db	721	MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETS FESMI	780
Qy	766	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	825
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	826	SNDDLFI SKEAQIRETETFS DSSPIEIIDEFPTLISSKTDSF SKLAREYTDLEVSHKSEI	885
Db	841	SNDDLFI SKEAQIRETETFS DSSPIEIIDEFPTLISSKTDSF SKLAREYTDLEVSHKSEI	900
Qy	886	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATS KVVLLPPDV SALGH	945
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATS KVVLLPPDV SALA-	959
Qy	946	TQAEIESIVKPKVLEKEAEKKLPSTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGV	1005

Db 960 TQAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGV 1019  
 Qy 1006 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDGHPFRAYLES 1065  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1020 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDGHPFRAYLES 1079  
 Qy 1066 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTTYVGALFNGLT 1125  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1080 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTTYVGALFNGLT 1139  
 Qy 1126 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1140 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192

RESULT 9

AAU33228

ID AAU33228 standard; protein; 1246 AA.

XX

AC AAU33228;

XX

DT 18-DEC-2001 (first entry)

XX

DE Novel human secreted protein #3719.

XX

KW Human; vaccination; gene therapy; nutritional supplement;  
 KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;  
 KW immune suppression; immune stimulation; anti-inflammatory; leukaemia.

XX

OS Homo sapiens.

XX

PN WO200179449-A2.

XX

PD 25-OCT-2001.

XX

PF 16-APR-2001; 2001WO-US008656.

XX

PR 18-APR-2000; 2000US-00552929.

PR 26-JAN-2001; 2001US-00770160.

XX

PA (HYSE-) HYSEQ INC.

XX

PI Tang YT, Liu C, Drmanac RT;

XX

DR WPI; 2001-611725/70.

XX

PT Nucleic acids encoding a range of human polypeptides, useful in genetic  
 PT vaccination, testing and therapy.

XX

PS Claim 20; Page 737; 765pp; English.

XX

CC The invention relates to novel human secreted polypeptides. The  
 CC polypeptides and antibodies to the polypeptides are useful for  
 CC determining the presence of or predisposition to a disease associated  
 CC with altered levels of polypeptide. The polypeptides are also useful for  
 CC identifying agents (agonists and antagonists) that bind to them. Cells  
 CC expressing the proteins are useful for identifying a therapeutic agent

CC for use in treatment of a pathology related to aberrant expression or  
 CC physiological interactions of the polypeptide. Vectors comprising the  
 CC nucleic acids encoding the polypeptides and cells genetically engineered  
 CC to express them are also useful for producing the proteins. The proteins  
 CC are useful in genetic vaccination, testing and therapy, and can be used  
 CC as nutritional supplements. They may be used to increase stem cell  
 CC proliferation; to regulate haematopoiesis; and in bone, cartilage, tendon  
 CC and/or nerve tissue growth or regeneration; immune suppression and/or  
 CC stimulation; as anti-inflammatory agents; and in treatment of leukaemias.  
 CC AAU29510-AAU33304 represent the amino acid sequences of novel human  
 CC secreted proteins of the invention  
 XX  
 SQ Sequence 1246 AA;

Query Match 93.3%; Score 5526.5; DB 4; Length 1246;  
 Best Local Similarity 93.0%; Pred. No. 1.5e-277;  
 Matches 1123; Conservative 13; Mismatches 39; Indels 33; Gaps 10;

Qy	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPED	60
Db	42	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPED	101
Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP	120
Db	102	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP	161
Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Db	162	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	221
Qy	181	SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP	226
		: : :	
Db	222	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP	281
Qy	227	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	286
Db	282	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	341
Qy	287	GSSFVSVPKAESAVIVANPREEIIIVKNKDEEEKLVSNILHXQQELPTALTCLVKEDEVV	346
Db	342	GSSFVSVPKAESAVIVANPREEIIIVKNKDEEEKLVSNILHNQQELPTALTCLVKEDEVV	401
Qy	347	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	406
Db	402	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	461
Qy	407	DKKCFADSLEQTNHEKDSSESSNDDTSFSPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	466
Db	462	DKKCFADSLEQTNHEKDSSESSNDDTSFSPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	521
Qy	467	PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTE	526
Db	522	PLLDGPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE	581
Qy	527	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	586
Db	582	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	641

Qy 587 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE 646  
 |||||  
 Db 642 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE 701  
 Qy 647 EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE 705  
 |||||  
 Db 702 EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSE 761  
 Qy 706 MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLVKESLTETSFESMI 765  
 |||||  
 Db 762 MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLVKESLTETSFESMI 821  
 Qy 766 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 825  
 |||||  
 Db 822 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 881  
 Qy 826 SNDDLFIKSEAQIRETETFSDDSPIEIIIDFPTLISSKTDSFSKLAREYTDLEVSHKSEI 885  
 |||||  
 Db 882 SNDDLFIKSEAQIRETETFSDDSPIEIIIDFPTLISSKTDSFSKLAREYTDLEVSHKSEI 941  
 Qy 886 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSA LGH 945  
 |||||  
 Db 942 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSA LA- 1000  
 Qy 946 TQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSA DLGKTSVVDLLYWRDIKKTGV 1005  
 ||||| : |||||  
 Db 1001 TQAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSA ELSKTSVVDLLYWRDIKKTGV 1060  
 Qy 1006 VFGAS-LFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAY-- 1062  
 |||| : |||||  
 Db 1061 VFGASAVFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAISG 1120  
 Qy 1063 -LESEVAISEELVQKYSNSALGHV-NCTIKELRR---LFLVDDLVDLSLKFVILMWVFTY 1116  
 ||| : : | : ||||| : ||| : | | ||||| : |||||  
 Db 1121 NLESCLYLRELGSGRYSNSALGSMWNCTVKGNFRAPSFWSMDLVDLSLRSFAVILMWVFTY 1180  
 Qy 1117 VGALFNGLTLL-----ILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 1170  
 || | || : | | : |||||  
 Db 1181 VGCL--GLMVLDTTGF WALNFISSSGSWLIYERHQAQIDHYLGLANKNVKDAMAKIQAKI 1238  
 Qy 1171 PGLKRKAE 1178  
 |||||  
 Db 1239 PGLKRKAE 1246

RESULT 10

ABU11573

ID ABU11573 standard; protein; 983 AA.

XX

AC ABU11573;

XX

DT 12-FEB-2003 (first entry)

XX

DE Human MDDT polypeptide SEQ ID 520.

XX

KW MDDT; human; disease detection and treatment molecule polypeptide;

KW anti-inflammatory; immunosuppressive; osteopathic; cytostatic; anti-HIV;  
 KW haemostatic; nephrotropic; antianaemic; antipsoriatic; hepatotropic;  
 KW gene therapy; protein replacement therapy; cell proliferative disorder;  
 KW cancer; adenocarcinoma; leukaemia; lymphoma; melanoma; myeloma; sarcoma;  
 KW anaemia; Crohn's disease; acquired immunodeficiency syndrome; AIDS;  
 KW Goodpasture's syndrome; inflammation; osteoporosis; thrombocytopaenia;  
 KW psoriasis; hepatitis.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200279449-A2.  
 XX  
 PD 10-OCT-2002.  
 XX  
 PF 27-MAR-2002; 2002WO-US009944.  
 XX  
 PR 28-MAR-2001; 2001US-0279619P.  
 PR 29-MAR-2001; 2001US-0280067P.  
 PR 29-MAR-2001; 2001US-0280068P.  
 PR 16-MAY-2001; 2001US-0291280P.  
 PR 17-MAY-2001; 2001US-0291829P.  
 PR 17-MAY-2001; 2001US-0291849P.  
 PR 19-JUN-2001; 2001US-0299428P.  
 PR 20-JUN-2001; 2001US-0299776P.  
 PR 20-JUN-2001; 2001US-0300001P.  
 XX  
 PA (INCY-) INCYTE GENOMICS INC.  
 XX  
 PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;  
 PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshey SR;  
 PI Daugherty SC, Dam TC, Liu TF, Nguyen DA, Kleefeld Y, Gerstin EH;  
 PI Peralta CH, David MH, Lewis SA, Chen AJ, Panzer SR, Harris B;  
 PI Flores V, Marwaha R, Lo A, Lan RY, Urashka ME;  
 XX  
 DR WPI; 2003-058431/05.  
 DR N-PSDB; ABX34563.  
 XX  
 PT New purified disease detection and treatment molecule proteins and  
 PT polynucleotides, useful for diagnosing, treating or preventing cancers  
 PT (e.g. leukemia or sarcoma), anemia, Crohn's disease, AIDS, osteoporosis  
 PT or hepatitis.  
 XX  
 PS Claim 27; SEQ ID NO 520; 339pp + Sequence Listing; English.  
 XX  
 CC This invention describes a novel disease detection and treatment molecule  
 CC polypeptide (MDDT) which has anti-inflammatory, immunosuppressive,  
 CC osteopathic, cytostatic, anti-HIV, haemostatic, nephrotropic,  
 CC antianaemic, antipsoriatic and hepatotropic activity. The polynucleotides  
 CC and the polypeptides of the invention can be used for gene therapy,  
 CC protein replacement therapy and are useful for treating a variety of  
 CC diseases or conditions. These polypeptides or polynucleotides are  
 CC particularly useful for diagnosing, treating or preventing cell  
 CC proliferative disorders (e.g. cancers including adenocarcinoma,  
 CC leukaemia, lymphoma, melanoma, myeloma or sarcoma), anaemia, Crohn's  
 CC disease, acquired immunodeficiency syndrome (AIDS), Goodpasture's  
 CC syndromes, inflammation, osteoporosis, thrombocytopaenia, psoriasis or  
 CC hepatitis. ABU11450-ABU11845 represent the MDDT polynucleotides encoded





Db 699 GSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPDVSALA-TQAEIES 757

Qy 953 IVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASLF 1012  
 ||||| :| |||||

Db 758 IVKPKVLVKEAEKKLPSDTEKEDRSPSAIFS AELSKTSVVDLLYWRDIKKTGVVFGASLF 817

Qy 1013 LLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEE 1072  
 |||||

Db 818 LLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEE 877

Qy 1073 LVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGFALFNGLTLLILALI 1132  
 |||||

Db 878 LVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGFALFNGLTLLILALI 937

Qy 1133 SLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178  
 |||||

Db 938 SLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 983

RESULT 11

AA95012

ID AAY95012 standard; protein; 893 AA.

XX

AC AAY95012;

XX

DT 19-JUN-2000 (first entry)

XX

DE Human secreted protein vb22\_1, SEQ ID NO:64.

XX

KW Human; secreted protein; cancer; tumour; cardiovascular disorder;  
 KW blood disorder; haemophilia; autoimmune disease; diabetes; inflammation;  
 KW infection; fungal; bacterial; viral; HIV; allergy; arthritis;  
 KW neurodegenerative disease; asthma; contraceptive.

XX

OS Homo sapiens.

XX

PN WO200011015-A1.

XX

PD 02-MAR-2000.

XX

PF 24-AUG-1999; 99WO-US019351.

XX

PR 24-AUG-1998; 98US-0097638P.

PR 24-AUG-1998; 98US-0097659P.

PR 09-SEP-1998; 98US-0099618P.

PR 28-SEP-1998; 98US-0102092P.

PR 25-NOV-1998; 98US-0109978P.

PR 23-DEC-1998; 98US-0113645P.

PR 23-DEC-1998; 98US-0113646P.

PR 23-AUG-1999; 99US-00379246.

XX

PA (ALPH-) ALPHAGENE INC.

XX

PI Valenzuela D, Yuan O, Hoffman H, Hall J, Rapiejko P;

XX

DR WPI; 2000-224657/19.

XX



Qy	586	FESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPY	645
Db	301	FESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPY	360
Qy	646	EEAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYS	704
Db	361	EEAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYS	420
Qy	705	EMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLKESLTETSFESM	764
Db	421	EMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLKESLTETSFESM	480
Qy	765	IEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAV	824
Db	481	IEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAV	540
Qy	825	YSNDDLFIKSEAQIRETETFSDDSPIEIIDEFPTLISSKTDIFSGLAREYTDLEVSHKSE	884
Db	541	YSNDDLFIKSEAQIRETETFSDDSPIEIIDEFPTLISSKTDIFSGLAREYTDLEVSHKSE	600
Qy	885	IANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATSQVLLLPDVSALG	944
Db	601	IANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATSQVLLLPDVSALA	660
Qy	945	HTQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTG	1004
Db	661	-TQAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSALSSTSVVDLLYWRDIKKTG	719
Qy	1005	VVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPPFRAYLE	1064
Db	720	VVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPPFRAYLE	779
Qy	1065	SEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGL	1124
Db	780	SEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGL	839
Qy	1125	TLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1178
Db	840	TLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	893

RESULT 12

AAY71310

ID AAY71310 standard; protein; 1163 AA.

XX

AC AAY71310;

XX

DT 02-NOV-2000 (first entry)

XX

DE Rat neurite growth inhibitor Nogo A.

XX

KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;  
 KW central nervous system; neoplastic disease; antiproliferative; glioma;  
 KW antisense gene therapy; neuroblastoma; meningioma; retinoblastoma;  
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;

KW structural plasticity; screening.

XX

OS Rattus sp.

XX

Feature	Key	Location/Qualifiers
FT	Inhibitory-site	1. .171
FT		/note= "Inhibits NIH 3T3 fibroblast spreading"
FT	Modified-site	30
FT		/note= "Casein kinase II site"
FT	Region	31. .58
FT		/note= "Acidic region"
FT	Region	31. .57
FT		/note= "Region specifically described in claim 16"
FT	Region	172. .259
FT		/note= "This region is not essential for inhibitory activity"
FT	Modified-site	233
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	242. .244
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	291
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	295
FT		/note= "Protein kinase C (PKC) site"
FT	Misc-difference	404
FT		/note= "Encoded by TTG"
FT	Modified-site	436
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	468. .470
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	484
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	488
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	502
FT		/note= "Casein kinase II site"
FT	Inhibitory-site	542. .722
FT	Modified-site	576
FT		/note= "Casein kinase II site"
FT	Peptide	623. .640
FT		/note= "used as immunogen to generate antibody AS 472"
FT	Modified-site	626
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	694. .696
FT		/note= "Asn is N-glycosylated"
FT	Modified-site	715
FT		/note= "Casein kinase II site"
FT	Peptide	762. .1163
FT		/note= "used as immunogen to generate antibody AS Bruna"
FT	Modified-site	784
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	821
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	850
FT		/note= "Protein kinase C (PKC) site"
FT	Modified-site	855
FT		/note= "Protein kinase C (PKC) site"

FT Modified-site 863  
 FT /note= "Casein kinase II site"  
 FT Modified-site 868  
 FT /note= "Protein kinase C (PKC) site"  
 FT Modified-site 893  
 FT /note= "Protein kinase C (PKC) site"  
 FT Modified-site 912. .914  
 FT /note= "Asn is N-glycosylated"  
 FT Modified-site 925. .927  
 FT /note= "Asn is N-glycosylated"  
 FT Modified-site 954  
 FT /note= "PKC and casein kinase II sites"  
 FT Modified-site 956  
 FT /note= "PKC and casein kinase II sites"  
 FT Region 975. .1162  
 FT /note= "This region is not essential for inhibitory  
 FT activity"  
 FT Region 976. .1163  
 FT /note= "C-terminal common region found in Nogo A, B and C  
 FT isoforms"  
 FT Domain 988. .1023  
 FT /label= Transmembrane\_domain  
 FT /note= "C-terminal hydrophobic region specifically  
 FT described in claim 16"  
 FT Modified-site 1024  
 FT /note= "Protein kinase C (PKC) site"  
 FT Modified-site 1071. .1073  
 FT /note= "Asn is N-glycosylated"  
 FT Modified-site 1073  
 FT /note= "Protein kinase C (PKC) site"  
 FT Modified-site 1089  
 FT /note= "Protein kinase C (PKC) site"  
 FT Domain 1090. .1125  
 FT /label= Transmembrane\_domain  
 FT /note= "C-terminal hydrophobic region specifically  
 FT described in claim 16"  
 FT Modified-site 1141. .1143  
 FT /note= "Asn is N-glycosylated"  
 FT Modified-site 1143  
 FT /note= "Protein kinase C (PKC) site"  
 XX  
 PN WO200031235-A2.  
 XX  
 PD 02-JUN-2000.  
 XX  
 PF 05-NOV-1999; 99WO-US026160.  
 XX  
 PR 06-NOV-1998; 98US-0107446P.  
 XX  
 PA (SCHW/) SCHWAB M E.  
 PA (CHEN/) CHEN M S.  
 XX  
 PI Schwab ME, Chen MS;  
 XX  
 DR WPI; 2000-400052/34.  
 DR N-PSDB; AAD01173.  
 XX

PT Nogo proteins and nucleic acids useful for treating neoplastic disorders  
PT of the central nervous system and inducing regeneration of neurons.

PS Claim 3; Fig 2A; 122pp; English.

The present sequence is a rat Nogo A protein which is a potent neural cell growth inhibitor and is free of all central nervous system (CNS) myelin material with which it is natively associated. The protein was derived from a cDNA generated by fusing R018U37-3, R1-3U21 cDNAs isolated from hexanucleotides-primed rat brain stem/spinal cord library, and Oli18 cDNA from an oligo d(T)-primed rat oligodendrocyte library. Nogo proteins and fragments displaying neurite growth inhibitory activity are used in the treatment of neoplastic disease of the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma, ependyoma, pinealoma, haemangioblastoma, acoustic neuroma, oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases. Therapeutics which promote Nogo activity can be used to treat or prevent hyperproliferative or benign dysproliferative disorders e.g. psoriasis and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be used to inhibit production of Nogo protein to induce regeneration of neurons or to promote structural plasticity of the CNS in disorders where neurite growth, regeneration or maintenance are deficient or desired. The animal models can be used in diagnostic and screening methods for predisposition to disorders and to screen for or test molecules which can treat or prevent disorders or diseases of the CNS. Note: The present sequence designated as SEQ ID NO: 2 is stated to be the same as the sequence shown in Fig. 13 (see AAY71384) of the specification. However, this sequence does not match the sequence given in Fig. 13. SEQ ID numbers 35-42 are referred in claim 32 and SEQ ID NO: 29 in disclosure of the specification. However, the specification does not include sequences for these SEQ ID numbers

XX

SQ Sequence 1163 AA;

Query Match 72.5%; Score 4296.5; DB 3; Length 1163;  
Best Local Similarity 74.0%; Pred. No. 6.2e-214;  
Matches 885; Conservative 104; Mismatches 156; Indels 51; Gaps 19;

72.5%; Score 4296.5; DB 3; Length 1163;

Best Local Similarity 74.0%; Pred. No. 6.2e-214;

Matches 885; Conservative 104; Mismatches 156; Indels 51; Gaps 19;

```
Qy      1 MEDLDQSPLVSSS--DSPPRPQPAFKYQFVREPEDEE-EEEEEEEEDEDEDLEELEVLERK  58  
        |||:||| ||||| ||||| ||||| ||||| ||||| :||:|
```

Db 1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEEDEEEEEDEEEDDEDLEELEVLERK 60

QY            59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVP    118  
| | | | | | | | | | | | : | : | | | | | | | | | | | | : | : |

Db 61 PAAGLSAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPEROPSWERSPAA---P 115

QY 119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPFPAPAPAAPSTPAAPKR 178

Db 116 APSLPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR 166

Qy 179 RGSSG-----AVVXXXXKIMDLKEQPNGTISAGQEDFPSVLLETAASXPSL 224  
||| : ||||| : : |||||

Db 167 RGSQSVDETLFALPAASEPVIPSSAEKIMDLMEQPGNTVSSGOEDFPSVLLETAASLPSL 226

Qy 225 SPLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYS 284  
 |||| ||||| ||||| | :|||:| :|||:| :| :|||

Db 227 SPLSTVSFKEHGYLGNL SAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYS 286

Qy 285 EMGSSFSVSPKAESAVIVANFREEIIVKNKDEEEKLVSNILHXQQELPTALTKLVKEDE 344  
 ||||| ||| |||::| | :||:|:|:|:|:| | : || || | |||

Db 287 EMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG-----KEDR 340

Qy 345 VVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNLE 403  
 ||| || | ||| ::| ||:|||||||: ||||: | | |:| | :|:

Db 341 VVSPEKTMDIFNEMQMSV VAPVREEYADFKPFQAWEVKDTYEGSRDVLAA----RANVE 396

Qy 404 SKVDKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIAT 463  
 ||||:| | |||| : |||| |:| ||||| :| | ||||| | :|||

Db 397 SKVDRKCIEDSLEQKSLGKDSEGRNEDASFPSTPEPVKDSRAYITCASFT-SATESTTA 455

Qy 464 NIFPLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLT 523  
 | ||||| |||| |||||:||||:| | || |||| | | |||| ||||| :|

Db 456 NTFPLLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFVAVQDSEADYVTTDTLSK 514

Qy 524 VTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLC 583  
 ||| |:||||||||||||||||| |||||:||||| :||||| |||

Db 515 VTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQLC 574

Qy 584 PSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEA-SSVNYESIKHEPENP 642  
 ||||:||||||||||||| :|||||:| | |||| |:|:| | ||||

Db 575 PSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPVSYDSIKLEPENP 634

Qy 643 PPYEEAMSVSLKVSGIKEEIKEPENINAAALQETEAPYISIACDLIKETKLSAEPAPDFSD 702  
 |||||:|:| | | | ||||: ||:||||||||||||||||| |:|:|:

Db 635 PPYEEAMNVALKALGTKEGIKEPESFNAAVQETEAPYISIACDLIKETKLSTEPSDFSN 694

Qy 703 YSEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIQVDPQKQDETVMVLKESLTETSFE 762  
 |||:| | |:|:|:|||||:|||||||||:| | |:| |||:||||| | |

Db 695 YSEIAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIQVDPQKQDEEAVMLKESLTEVS-E 753

Qy 763 SMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELST 822  
 :: :: :|:| | | |||||: :| :| | :: ||:| | | | | :|

Db 754 TVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLQMEEFNT 811

Qy 823 AVYSNDDLFIKSEAQIRETETFSDDSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHK 882  
 |:| | | | | :|:|:||||| |||||:|:| | | | | | | | |

Db 812 AIYSNDDLSSKEDKIKESETFSDDSPIEIIDEFPTFVSAKDDS-PKLAKEYTDLEVSDK 870

Qy 883 SEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATS KVL LPPDVSA 942  
 |||| | | ||| || | || | || | | :|: | | :| | :| |

Db 871 SEIANIQSGADSLPCLELPCLDSFKNIYPK--DEVHVSDEFSENRSSVSKASISPSNVSA 928

Qy 943 LGHTQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIK 1002  
 | | |:| | | | ||||| ||||| ||: ||: | |||||

Db 929 L-EPQTEMGSIVKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIK 987

Qy 1003 TGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAY 1062  
 |||||

Db 988 TGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAY 1047

Qy 1063 LESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFN 1122  
 |||||

Db 1048 LESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFN 1107

QY 1123 GLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178  
 |||||:||||| |||||:|||||:  
 Db 1108 GLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 1163

RESULT 13

ABB81074

ID ABB81074 standard; protein; 1163 AA.

XX

AC ABB81074;

XX

DT 05-NOV-2002 (first entry)

XX

DE Rat neurotransmitter receptor protein Nogo-A.

XX

KW Nerve regeneration; neuroprotection; neuronal degeneration; CNS; PNS;  
 KW central nervous system; peripheral nervous system; tranquillizer; Nogo;  
 KW vulnerary; cerebroprotective; anti-tumour; antidiabetic; anticonvulsant;  
 KW nootropic; antiparkinsonian; ophthalmological; analgesic; hepatotropic;  
 KW osteopathic; vasotropic; nephrotropic; cytostatic; antigen; gene therapy;  
 KW neurotransmitter receptor; rat; receptor.

XX

OS Rattus norvegicus.

XX

PN US2002072493-A1.

XX

PD 13-JUN-2002.

XX

PF 28-JUN-2001; 2001US-00893348.

XX

PR 19-MAY-1998; 98IL-00124500.

PR 21-JUL-1998; 98WO-US014715.

PR 22-DEC-1998; 98US-00218277.

PR 19-MAY-1999; 99US-00314161.

XX

PA (YEDA ) YEDA RES & DEV CO LTD.

XX

PI Eisenbach-Schwartz M, Hauben E, Cohen IR, Beserman P, Mosonego A;  
 PI Moalem G;

XX

DR WPI; 2002-607255/65.

DR N-PSDB; ABN86600.

XX

PT Promoting nerve regeneration and preventing neuronal degeneration in the  
 PT central/peripheral nervous system from injury/disease, comprises  
 PT administering nervous system-specific activated T cells/antigen, or  
 PT analogs/peptides.

XX

PS Example 5; Page 44-47; 93pp; English.

XX

CC The invention relates to promoting nerve regeneration or conferring  
 CC neuroprotection and preventing or inhibiting neuronal degeneration in the  
 CC central/peripheral nervous system (NS). The method involves administering  
 CC NS-specific activated T cells, NS-specific antigen, its analogue or its  
 CC peptide, a nucleotide sequence the NS-specific antigen or its analogue or  
 CC combinations. The method is useful for promoting nerve regeneration and



CC preventing neuronal degeneration in central/peripheral nervous system  
 CC from injury/disease, where the injury is spinal cord injury, blunt  
 CC trauma, penetrating trauma, hemorrhagic stroke, ischaemic stroke or  
 CC damages caused by surgery such as tumour excision. The disease is not an  
 CC autoimmune disease or neoplasm. The disease results in a degenerative  
 CC process occurring in either gray or white matter or both. The disease is  
 CC diabetic neuropathy, senile dementia, Alzheimer's disease, Parkinson's  
 CC disease, facial nerve (Bell's) palsy, glaucoma, Huntington's chorea,  
 CC amyotrophic lateral sclerosis, non-arteritic optic neuropathy, and  
 CC vitamin deficiency, intervertebral disc herniation, prion diseases such  
 CC as Creutzfeldt-Jakob disease, carpal tunnel syndrome, peripheral  
 CC neuropathies associated with various diseases, including but not limited  
 CC to uremia, porphyria, hypoglycemia, Sjorgren Larsson syndrome, acute  
 CC sensory neuropathy, chronic ataxic neuropathy, biliary cirrhosis, primary  
 CC amyloidosis, obstructive lung diseases, acromegaly, malabsorption  
 CC syndromes, polycythemia vera, immunoglobulin (Ig)A- and IgG gamma-  
 CC pathies, complications of various drugs (e.g., metronidazole) and toxins  
 CC (e.g., alcohol or organophosphates), Charcot-Marie-Tooth disease, ataxia  
 CC telangectasia, Friedreich's ataxia, amyloid polyneuropathies,  
 CC adrenomyeloneuropathy, Giant axonal neuropathy, Refsum's disease, Fabry's  
 CC disease, or lipoproteinemia. The present sequence represents the rat  
 CC neurotransmitter receptor protein Nogo-A, an example of NS-specific  
 CC antigen

XX

SQ Sequence 1163 AA;

Query Match 72.5%; Score 4296.5; DB 5; Length 1163;  
 Best Local Similarity 74.0%; Pred. No. 6.2e-214;  
 Matches 885; Conservative 104; Mismatches 156; Indels 51; Gaps 19;

Qy	1	MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEE-EEEEEEEEDEDEDLEELEVLERK	58
		:	
Db	1	MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEDEEEEEEEEEDEDEDLEELEVLERK	60
Qy	59	PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSSSTVP	118
Db	61	PAAGLSAAAVP--PAAAAPLLDFSSDSVPPAPRGPLPAAPPAAPERQPSWERSPA--P	115
Qy	119	APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEFVWTPPAPAPAAPPSTPAAPKR	178
Db	116	APSLPPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR	166
Qy	179	RGSSG-----AVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSL	224
		:	
Db	167	RGSGSVDETLFALPAASEPVISSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSL	226
Qy	225	SPLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYS	284
		:       :     :           :     :	
Db	227	SPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYS	286
Qy	285	EMGSSFSVSPKAESAVIVANPREEIIIVKNKDEEEKLVSNILHXQQELPTALTCLKVKEDE	344
		:     :     :     :     :	
Db	287	EMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPGV-----KEDR	340
Qy	345	VVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNLE	403
		: :     :           :       :         :	
Db	341	VVSPEKTMDFNEMQMSVAVPREEYADFKPFQAWEVKDTYEGSRDVLAA---RANVE	396



XX  
 AC AAY71557;  
 XX  
 DT 02-NOV-2000 (first entry)  
 XX  
 DE Rat Nogo A truncated protein used in the construction of mutant Nogo-A.  
 XX  
 KW Rat; neurite growth inhibitor; Nogo A; neural cell; myelin; CNS;  
 KW central nervous system; neoplastic disease; antiproliferative; glioma;  
 KW antisense gene therapy; neuroblastoma; menagioma; retinoblastoma;  
 KW degenerative nerve disease; Alzheimer's disease; Parkinson's disease;  
 KW hyperproliferative disorder; benign dysproliferative disorder; diagnosis;  
 KW psoriasis; tissue hypertrophy; neuronal regeneration; treatment;  
 KW structural plasticity; screening; mutant; mutein.  
 XX  
 OS Rattus sp.  
 XX  
 PN WO200031235-A2.  
 XX  
 PD 02-JUN-2000.  
 XX  
 PF 05-NOV-1999; 99WO-US026160.  
 XX  
 PR 06-NOV-1998; 98US-0107446P.  
 XX  
 PA (SCHW/) SCHWAB M E.  
 PA (CHEN/) CHEN M S.  
 XX  
 PI Schwab ME, Chen MS;  
 XX  
 DR WPI; 2000-400052/34.  
 XX  
 PT Nogo proteins and nucleic acids useful for treating neoplastic disorders  
 PT of the central nervous system and inducing regeneration of neurons.  
 XX  
 PS Example; Page; 122pp; English.  
 XX  
 CC The patent relates to neurite growth inhibitor Nogo which is free of all  
 CC central nervous system (CNS) myelin material with which it is natively  
 CC associated. Nogo proteins and fragments displaying neurite growth  
 CC inhibitory activity are used in the treatment of neoplastic disease of  
 CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,  
 CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,  
 CC oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and  
 CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.  
 CC Therapeutics which promote Nogo activity can be used to treat or prevent  
 CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis  
 CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be  
 CC used to inhibit production of Nogo protein to induce regeneration of  
 CC neurons or to promote structural plasticity of the CNS in disorders where  
 CC neurite growth, regeneration or maintenance are deficient or desired. The  
 CC animal models can be used in diagnostic and screening methods for  
 CC predisposition to disorders and to screen for or test molecules which can  
 CC treat or prevent disorders or diseases of the CNS. The present sequence  
 CC is a truncated form of rat Nogo A protein shown in AAY71310, which is  
 CC used in the construction of mutant Nogo-A. Nogo-A is composed of His-  
 CC tag/T7-tag/vector/Nogo-A sequence aa 1-1162. Nogo A deletion mutants were





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XX
OS   Rattus sp.
XX
FH   Key          Location/Qualifiers
FT   Inhibitory-site 1. .171
FT                               /note= "Inhibits NIH 3T3 fibroblast spreading"
FT   Modified-site   30
FT                               /note= "Casein kinase II site"
FT   Region          31. .58
FT                               /note= "Acidic region"
FT   Region          172. .259
FT                               /note= "This region is not essential for inhibitory
FT                               activity"
FT   Misc-difference 223
FT                               /label= Unknown
FT                               /note= "There is Leu at this position in the sequence
FT                               shown in AAY71310"
FT   Modified-site   233
FT                               /note= "Protein kinase C (PKC) site"
FT   Modified-site   242. .244
FT                               /note= "Asn is N-glycosylated"
FT   Modified-site   291
FT                               /note= "Protein kinase C (PKC) site"
FT   Modified-site   295
FT                               /note= "Protein kinase C (PKC) site"
FT   Misc-difference 404
FT                               /note= "There is Ile at this position in the sequence
FT                               shown in AAY71310"
FT   Modified-site   436
FT                               /note= "Protein kinase C (PKC) site"
FT   Modified-site   468. .470
FT                               /note= "Asn is N-glycosylated"
FT   Misc-difference 469
FT                               /label= Unknown
FT                               /note= "There is Lys at this position in the sequence
FT                               shown in AAY71310"
FT   Modified-site   484
FT                               /note= "Protein kinase C (PKC) site"
FT   Modified-site   488
FT                               /note= "Protein kinase C (PKC) site"
FT   Modified-site   502
FT                               /note= "Casein kinase II site"
FT   Inhibitory-site 542. .722
FT   Modified-site   576
FT                               /note= "Casein kinase II site"
FT   Peptide         623. .640
FT                               /note= "used as immunogen to generate antibody AS 472"
FT   Modified-site   626
FT                               /note= "Protein kinase C (PKC) site"
FT   Misc-difference 661
FT                               /note= "There is Asn at this position in the sequence
FT                               shown in AAY71310"
FT   Modified-site   694. .696
FT                               /note= "Asn is N-glycosylated"
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FT                               /note= "Casein kinase II site"
FT   Peptide         762. .1163

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FT /note= "used as immunogen to generate antibody AS Bruna"  
 FT Modified-site 784  
 FT /note= "Protein kinase C (PKC) site"  
 FT Misc-difference 820  
 FT /note= "There is Leu at this position in the sequence  
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 FT Modified-site 850  
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 FT /note= "C-terminal hydrophobic region"  
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 PN WO200031235-A2.  
 XX  
 PD 02-JUN-2000.  
 XX  
 PF 05-NOV-1999; 99WO-US026160.  
 XX

PR 06-NOV-1998; 98US-0107446P.

XX

PA (SCHW/) SCHWAB M E.

PA (CHEN/) CHEN M S.

XX

PI Schwab ME, Chen MS;

XX

DR WPI; 2000-400052/34.

XX

PT Nogo proteins and nucleic acids useful for treating neoplastic disorders  
PT of the central nervous system and inducing regeneration of neurons.

XX

PS Claim 3; Fig 13; 122pp; English.

XX

CC The present sequence is an alternative version of rat Nogo A protein  
CC which is a potent neural cell growth inhibitor and is free of all central  
CC nervous system (CNS) myelin material with which it is natively  
CC associated. Nogo proteins and fragments displaying neurite growth  
CC inhibitory activity are used in the treatment of neoplastic disease of  
CC the CNS e.g. glioma, glioblastoma, medulloblastoma, craniopharyngioma,  
CC ependyoma, pinealoma, haemangioblastoma, acoustic neuroma,  
CC oligodendroglioma, menagioma, neuroblastoma or retinoblastoma and  
CC degenerative nerve diseases e.g. Alzheimer's and Parkinson's diseases.  
CC Therapeutics which promote Nogo activity can be used to treat or prevent  
CC hyperproliferative or benign dysproliferative disorders e.g. psoriasis  
CC and tissue hypertrophy. Ribozymes or antisense Nogo nucleic acids can be  
CC used to inhibit production of Nogo protein to induce regeneration of  
CC neurons or to promote structural plasticity of the CNS in disorders where  
CC neurite growth, regeneration or maintenance are deficient or desired. The  
CC animal models can be used in diagnostic and screening methods for  
CC predisposition to disorders and to screen for or test molecules which can  
CC treat or prevent disorders or diseases of the CNS. Note: The present  
CC sequence is an alternative version of the Nogo A sequence shown in Fig.  
CC 2A (see AAY71310). SEQ ID numbers 35-42 are referred in claim 32 and SEQ  
CC ID NO: 29 in disclosure of the specification. However the specification  
CC does not include sequences for these SEQ ID numbers

XX

SQ Sequence 1163 AA;

Query Match 72.4%; Score 4286.5; DB 3; Length 1163;

Best Local Similarity 74.1%; Pred. No. 2.1e-213;

Matches 886; Conservative 104; Mismatches 155; Indels 51; Gaps 19;

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Qy 404 SKVDKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIAT 463  
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Qy 464 NIFPLLEDPTSENXTDEKKIEEKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTK 523  
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Qy 524 VTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLC 583  
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Db 812 AIYSNDDLSSSKEDKIKESETFSDDSPIEIIDFPTFVSAKDDS-PKLAKEYTDLEVSDK 870

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Db 929 L-EPQTEMGSIKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIK 987

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Db 988 TGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAY 1047

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 Job time : 108.384 secs

OM protein - protein search, using sw model

Run on: September 29, 2004, 18:09:33 ; Search time 29.2441 Seconds  
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Perfect score: 5923  
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Scoring table: BLOSUM62  
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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	%		DB	ID	Description
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1	931	15.7	199	2	US-08-700-607-1	Sequence 1, Appli
2	787.5	13.3	776	2	US-08-700-607-5	Sequence 5, Appli
3	705	11.9	356	2	US-08-700-607-6	Sequence 6, Appli
4	688	11.6	208	2	US-08-700-607-7	Sequence 7, Appli
5	671	11.3	267	2	US-08-700-607-8	Sequence 8, Appli
6	541.5	9.1	168	4	US-09-149-476-563	Sequence 563, App
7	513	8.7	241	2	US-08-700-607-3	Sequence 3, Appli
8	344.5	5.8	75	4	US-09-621-976-4600	Sequence 4600, Ap
9	344.5	5.8	75	4	US-09-621-976-4601	Sequence 4601, Ap
10	316	5.3	8991	4	US-08-714-741-32	Sequence 32, Appl
11	296.5	5.0	2468	4	US-09-976-594-726	Sequence 726, App

12	285	4.8	92	4	US-09-149-476-411	Sequence 411, App
13	276.5	4.7	1786	3	US-08-973-462-8	Sequence 8, Appli
14	267.5	4.5	1601	4	US-09-345-473E-40	Sequence 40, Appl
15	265	4.5	1596	4	US-08-978-277A-4	Sequence 4, Appli
16	263.5	4.4	2409	6	5180808-2	Patent No. 5180808
17	256	4.3	1780	1	US-08-769-309A-5	Sequence 5, Appli
18	256	4.3	1780	3	US-08-994-570-5	Sequence 5, Appli
19	238	4.0	1346	2	US-08-635-121-2	Sequence 2, Appli
20	238	4.0	1346	4	US-08-978-277A-2	Sequence 2, Appli
21	237.5	4.0	688	3	US-09-141-047-8	Sequence 8, Appli
22	237.5	4.0	1270	4	US-07-757-022B-44	Sequence 44, Appl
23	237.5	4.0	1311	4	US-07-757-022B-42	Sequence 42, Appl
24	237.5	4.0	1313	4	US-07-757-022B-142	Sequence 142, App
25	237.5	4.0	1314	4	US-07-757-022B-50	Sequence 50, Appl
26	237.5	4.0	1320	4	US-07-757-022B-46	Sequence 46, Appl
27	237.5	4.0	1320	4	US-07-757-022B-60	Sequence 60, Appl
28	237.5	4.0	1354	4	US-07-757-022B-48	Sequence 48, Appl
29	237.5	4.0	1361	4	US-07-757-022B-40	Sequence 40, Appl
30	237.5	4.0	1363	4	US-07-757-022B-52	Sequence 52, Appl
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32	237.5	4.0	1404	4	US-07-757-022B-62	Sequence 62, Appl
33	234.5	4.0	941	4	US-07-757-022B-14	Sequence 14, Appl
34	234.5	4.0	1022	4	US-07-757-022B-84	Sequence 84, Appl
35	234.5	4.0	1038	4	US-07-757-022B-74	Sequence 74, Appl
36	234.5	4.0	1049	4	US-07-757-022B-58	Sequence 58, Appl
37	234.5	4.0	1140	4	US-07-757-022B-104	Sequence 104, App
38	233.5	3.9	1320	4	US-10-164-595-58	Sequence 58, Appl
39	233.5	3.9	1404	4	US-10-164-595-78	Sequence 78, Appl
40	233.5	3.9	2137	4	US-09-134-001C-4463	Sequence 4463, Ap
41	228	3.8	977	4	US-09-010-147B-18	Sequence 18, Appl
42	226.5	3.8	630	3	US-08-973-462-9	Sequence 9, Appli
43	225.5	3.8	2954	4	US-09-150-867-1	Sequence 1, Appli
44	225	3.8	783	6	5231168-2	Patent No. 5231168
45	225	3.8	3256	4	US-09-919-172-98	Sequence 98, Appl

#### ALIGNMENTS

##### RESULT 1

US-08-700-607-1

; Sequence 1, Application US/08700607

; Patent No. 5858708

##### ; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Au-Young, Janice

; APPLICANT: Goli, Surya K.

; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

; NUMBER OF SEQUENCES: 9

##### ; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: U.S.

; ZIP: 94304



```

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/700,607
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0114 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 776 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 307307
US-08-700-607-5

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Query Match          13.3%; Score 787.5; DB 2; Length 776;
Best Local Similarity 31.9%; Pred. No. 3.6e-40;
Matches 229; Conservative 91; Mismatches 190; Indels 207; Gaps 25;

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Qy      588 ESEATPSPVLPDI--VMEAPLNSA-----VPSAGASVIQPSSSPLE---ASSVNY---- 632
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Db      141 EELGTPGPSLPDVPGIESRGLFSSDSGIEMTPAESTEVNKKILADPLDQMKAEAYKYIDIT 200

Qy      633 --ESIKHEPENPPPYEEA-----MSVSLKVSGIKEEIKEPENINAAL-----QET 675
      | :||: :: | |:          :|| |::| | | : : : |
Db      201 RPVEEVKHQEQHHPELEDKDLDFKNKDTDISIKPEGVREPDK-PAPVEGKIIKDHLLEEST 259

Qy      676 EAPYISIIACDL-----IKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELVED 722
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Db      260 FAPYID---DLSEEQRRAPQITTPVKITLTEIPEPSVE-----TTTQEKTPKQDICKL 309

Qy      723 SSPDSEPVDLFS---DDS-----IPDVPQKQ-----DETVMLVKESLTETSF 761
      |||: |  |  |||          | : |          || : :||:
Db      310 PSPDTVPTVTVSEPEDDSPGSITPPSSGTEPSAAESQGKGSISEDELITAIKEA----- 363

Qy      762 ESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELS 821

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US-08-700-607-6

Matches 168; Conservative 55; Mismatches 86; Indels 85; Gaps 11;

Db 323 QAQIDQYLGLVRTHINAVVAKIQAKIPGAKRHAE 356

; Patent No. 5858708





QY 1168 AKIPGLKRKAE 1178  
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Db 198 AKIPGAKRHAE 208

RESULT 5

US-08-700-607-8

; Sequence 8, Application US/08700607

; Patent No. 5858708

; GENERAL INFORMATION:

; APPLICANT: Bandman, Olga

; APPLICANT: Au-Young, Janice

; APPLICANT: Goli, Surya K.

; APPLICANT: Hillman, Jennifer L.

; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS

; NUMBER OF SEQUENCES: 9

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Incyte Pharmaceuticals, Inc.

; STREET: 3174 Porter Drive

; CITY: Palo Alto

; STATE: CA

; COUNTRY: U.S.

; ZIP: 94304

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/700,607

; FILING DATE: Filed Herewith

; ATTORNEY/AGENT INFORMATION:

; NAME: Billings, Lucy J.

; REGISTRATION NUMBER: 36,749

; REFERENCE/DOCKET NUMBER: PF-0114 US

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 415-855-0555

; TELEFAX: 415-845-4166

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 267 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

; IMMEDIATE SOURCE:

; LIBRARY: GenBank

; CLONE: 281046

US-08-700-607-8

Query Match 11.3%; Score 671; DB 2; Length 267;

Best Local Similarity 66.3%; Pred. No. 1.1e-33;

Matches 124; Conservative 34; Mismatches 29; Indels 0; Gaps 0;

QY 988 KTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKQVI 1047  
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Db 9 KSQAIDLLYWRDIKQTGIVFGSFLLLLSLTQFSVSVVAYLALAALSATISFRIYKSVL 68



; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,592  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,581  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,584  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,500  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,587  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,492  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,598  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,613  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,582  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,596  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,612  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,632  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,601  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/043,580  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,568  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,314  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,569  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,311  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,671  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,674  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,669  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,312  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,313  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,672  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,315  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/048,974  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/056,886  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,877  
; EARLIER FILING DATE: 1997-08-22

; EARLIER APPLICATION NUMBER: 60/056,889  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,893  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,630  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,878  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,662  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,872  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,882  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,637  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,903  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,888  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,879  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,880  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,894  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,911  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,636  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,874  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,910  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,864  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,631  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,845  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,892  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/057,761  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/047,595  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,599  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,588  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,585  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,586  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,590  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,594

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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,593
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02
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Query Match          9.1%; Score 541.5; DB 4; Length 168;
Best Local Similarity 60.5%; Pred. No. 5e-26;
Matches 101; Conservative 34; Mismatches 31; Indels 1; Gaps 1;
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Qy      1013 LLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEE 1072
          :|||  ||:|  |:  |||||  |||:|  |||:|  |||:  ::  :|  |
Db      1 MLLSLAAFSVISVVSYLILALLSVTISFRIYKSVIQAVQKSEEGHPFKAYLDVDITLSSE 60

Qy      1073 LVQKYSNSALGHVNCTIKELRRFLVDDLVDLSLKFAVLMWVFETYVGALFNGLTLLILALI 1132
          |  |:  |:  |:  :  ||||:  |||||  ||  ||:  ||||:  |||:  |||||  :
Db      61 AFHNYMNAAMVHINRALKLIIRLFLVEDLVDLSLKLAVFWMWLMTYVGAVFNGITLLILAE 120
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Qy 1133 SLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGL-KRKAE 1178  
 :||||:||||: |||||:| | : |||||:|: ||||  
 Db 121 LIFSVPIVYEKYKTQIDHYVGIARDQTKSIVEKIQAKLPGIAKKKAE 167

RESULT 7

US-08-700-607-3

; Sequence 3, Application US/08700607  
 ; Patent No. 5858708  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bandman, Olga  
 ; APPLICANT: Au-Young, Janice  
 ; APPLICANT: Goli, Surya K.  
 ; APPLICANT: Hillman, Jennifer L.  
 ; TITLE OF INVENTION: TWO NOVEL HUMAN NSP-LIKE PROTEINS  
 ; NUMBER OF SEQUENCES: 9  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
 ; STREET: 3174 Porter Drive  
 ; CITY: Palo Alto  
 ; STATE: CA  
 ; COUNTRY: U.S.  
 ; ZIP: 94304  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Diskette  
 ; COMPUTER: IBM Compatible  
 ; OPERATING SYSTEM: DOS  
 ; SOFTWARE: FastSEQ Version 1.5  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/700,607  
 ; FILING DATE: Filed Herewith  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Billings, Lucy J.  
 ; REGISTRATION NUMBER: 36,749  
 ; REFERENCE/DOCKET NUMBER: PF-0114 US  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415-855-0555  
 ; TELEFAX: 415-845-4166  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 241 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: peptide  
 ; IMMEDIATE SOURCE:  
 ; LIBRARY: THP1NOB01  
 ; CLONE: 31870  
 US-08-700-607-3

Query Match 8.7%; Score 513; DB 2; Length 241;  
 Best Local Similarity 47.7%; Pred. No. 4.7e-24;  
 Matches 102; Conservative 37; Mismatches 55; Indels 20; Gaps 1;

Qy 963 AEKKLPDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSI 1022  
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Query Match          5.8%; Score 344.5; DB 4; Length 75;
Best Local Similarity 82.6%; Pred. No. 1.9e-14;
Matches 71; Conservative 0; Mismatches 4; Indels 11; Gaps 1;

Qy          1 MEDLDQSPLVSSSDSPPRQPQAFKYQFVREPEDEEEEEEEEEDEDEDLEEELEVLERKPA 60
             ||||||||||||||||||| ||||||| ||||||| |||||||
Db          1 MEDLDQSPLVSSSDSPPRXQPAFKYQFXREPEDEE-----EDLEEELEVLERKPA 49

Qy          61 AGLSAAPVPTAPAAGAPLMDFGNDFV 86

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Db                    ||| |||| |||||||||||||||  
50 AGLXAAPVXTAPAAGAPLMDFGNDFV 75

RESULT 9

US-09-621-976-4601  
; Sequence 4601, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 4601  
; LENGTH: 75  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 58  
; OTHER INFORMATION: Xaa = His,Pro  
; NAME/KEY: UNSURE  
; LOCATION: 28  
; OTHER INFORMATION: Xaa = Met,Val  
; NAME/KEY: UNSURE  
; LOCATION: 19  
; OTHER INFORMATION: Xaa = Pro,Gln  
; NAME/KEY: UNSURE  
; LOCATION: 53  
; OTHER INFORMATION: Xaa = Ser,Tyr  
US-09-621-976-4601

Query Match                    5.8%; Score 344.5; DB 4; Length 75;  
Best Local Similarity       82.6%; Pred. No. 1.9e-14;  
Matches    71; Conservative    0; Mismatches    4; Indels    11; Gaps    1;

QY            1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60  
              |||||||||||||||| ||||||| |||||||                |||||||||||||  
Db            1 MEDLDQSPLVSSSDSPPRXQPAFKYQFXREPEDEE-----EDLEELEVLERKPA 49  
  
QY            61 AGLSAAPVPTAPAAGAPLMDFGNDFV 86  
              ||| |||| |||||||||||||||||  
Db            50 AGLXAAPVXTAPAAGAPLMDFGNDFV 75

RESULT 10

US-08-714-741-32  
; Sequence 32, Application US/08714741  
; Patent No. 6500613  
; GENERAL INFORMATION:  
; APPLICANT: Briles, David E.  
; APPLICANT: McDaniel, Larry S.

```

; APPLICANT: Swiatlo, Edwin
; APPLICANT: Yother, Janet
; APPLICANT: Crain, Marilyn J.
; APPLICANT: Hollingshead, Susan
; APPLICANT: Tart, Rebecca
; APPLICANT: Brooks-Walter, Alexis
; TITLE OF INVENTION: PNEUMOCOCCAL GENES, PORTIONS THEREOF,
; TITLE OF INVENTION: EXPRESSION PRODUCTS THEREFROM, AND USES OF SUCH GENES,
; TITLE OF INVENTION: PORTIONS AND PRODUCTS
; NUMBER OF SEQUENCES: 47
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Curtis, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/714,741
; FILING DATE: 16-SEP-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer Esq., William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454312-2460
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8991 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
US-08-714-741-32

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Query Match          5.3%; Score 316; DB 4; Length 8991;
Best Local Similarity 21.4%; Pred. No. 9.9e-10;
Matches 248; Conservative 138; Mismatches 479; Indels 296; Gaps 52;

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Qy      6 QSPLVSSDSP-PRPQPAFKYQF-VREPEDEEEEEEEEEDEDEDLEE--LEVLERKPAA 61
      ::|      :| ||| | :      :|: |: :::: |||      ||      : ::::|
Db      7193 EAPAEQPKPAPAPQAPAPKPEKPAPAEQPKPEKTDDQQAEDYARRSEEEYNRLTQQQPPK 7252

Qy      62 GLSAAPVP-----TAPAAG-----APLMDF 81
      || |      | | |      | |
Db      7253 AEKPAPAPKTGWKQENGWYFYNTDGSMGEQAGQYRAAAEGDLAAKQAELEKTEADLKKA 7312

Qy      82 GNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSPVSTVPAPSPLSAAAVSPSKLPED---DE 138
      |: ||| || | || || |:| ||| | |      :: :| :|
Db      7313 VNEPEKPAPAPETPA--PEAPAEQPK--PAPAPQAPAPKPEKPAPAEQPKAEKTDDQQAEE 7368

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QY 139 PPAR-----PPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKRRGSSGAVVXXX 189  
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 Db 7369 DYARRSEEEYNRLTQQQPPKAEKPAPAPKPEQPAPAPKNSKGEQAEQYRSAAGGDIAAKQ 7428  
 QY 190 XKI----MDLKEQPGNTISAGQEDFPSVLLET-AASXPSLSPLSAASFKEHEYLGNLSTV 244  
 :: |||: : : : | : || | | : | : :  
 Db 7429 VELEKTEADLKK-----AVNEPEKPAPAPETPAPEAPAEQPKPAPAPQ----- 7471  
 QY 245 LPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSFSVSPKAESAVIVAN 304  
 | :| | :|| : | || ||: : : ||||  
 Db 7472 -PAPAPKPEKPAEQPK--AEKPADQQAEEDYDRRSEEEYNRL--TQQQPPKAEKPAPAPQ 7526  
 QY 305 PREEI-----IVKNKDEEEKLVSNNILHXQQELPTALTCLVKEDEVVSSEKAKDSFNE 357  
 | : : | : : | || || | :| :| :|  
 Db 7527 PEQPAPAPKSLKEIDESDSEDYVKEGFRAPLQSELDKQAKLSKLEEL-----SDKIDE 7580  
 QY 358 KRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDDKCFADSLEQ 417  
 : | : : ||| || || : : | : || |||  
 Db 7581 LDAEI-AKLEKDVEDFK-----XSDGEQAGQYLAAAEEDLIAKKA---ELEQ 7623  
 QY 418 TNHEKDSESSNDDTSFPS---TPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTS 474  
 | | | : : : : | : || || || |  
 Db 7624 T--EADLKKAVNEPGKPAPAPAE-----TPAPEAPAEQPK-----PAP 7660  
 QY 475 ENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYV--TTDNLTKVTEEVVA-- 530  
 | | : | | || | | :| || : : : :|  
 Db 7661 ETPAPAPKPEKPAEQPKPEK-----PADQQAEEDYARRSEEEYNRLTQQQPAPA 7709  
 QY 531 -----NMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSSEVMQESLYPAAQLCP 584  
 || : | : : : : : | | | || : : |  
 Db 7710 QKPEQPAKPEKPAEPTQPEKDAEIAKLE-KNVEYFKKTDAEQTEQYLAAAEKDLADKKA 7768  
 QY 585 SFESEA-----TPSPV-LPDIVMEAPLNSAVPSAGASVIQPSSSPLEAS 628  
 | :|| ||:| | : | | : | : : :  
 Db 7769 ELEKTEADLKKAVNEPEKPAEETPAPAPKPEQPAEQPKPAPAPQP-APAPKPEKTDQQA 7827  
 QY 629 SVNYESIKHEPENPPPYEEAMSVSLKVSGIKEE----IKEPENINAALQETEAPYISIA 684  
 :| | | | : : | | : ||| || : |  
 Db 7828 EEDYARRSEEEYNRLPQQQPPKAEKPAPAPKPEQPVPAEXPEN-----PAPAPKPAXAP 7881  
 QY 685 DLIKETKLSAEPAPDFSDYSEMAKVEQPV-----PDHSELVEDSS-----PDS 727  
 :| : : :| | : | :| || : || : |  
 Db 7882 QPLKPEEPAEQPKPE-----KPEEPAGQPEPEKPDQQAGEDYARRSGGEYNRFPQQ 7933  
 QY 728 EPVDLFSDDSI PDVPQKQDETVMVLVKESTETSFESMIEYENKEKLSALPPEGG----- 781  
 :| | | : : | | | | ||: :  
 Db 7934 QPPKAEKPAPAP----KPEQVPAPAKTLL-----KKAKLAGAKSKAATKKAEL 7977  
 QY 782 KPYLESFKLSLDNTKDTLLP-----DEV-----STLSKK-EKIPLQMEELSTAVYSNDD 829  
 :| || : | :| || | ||: : | :| | :| :| :|  
 Db 7978 EPELEKAEAELENLLSTLDPEGKTQDELDKAEAEALNKKVEALPNQVSELEEELSKLED 8037  
 QY 830 LFISKEAQIRETETFSDDSSPIEIIDEFPTLISSKTDSEFSKLARE----YTDLEVSHKSEI 885  
 | :| : | : | :| :| :| :| :|  
 Db 8038 NL--KDAETNNVEDY-----IKEGLEEAIATKQAELEKTPKELDAALNELGPDGDEEE 8088

Qy 886 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKI--SFSDDFSKNGSATSKVLLLPDVSAL 943  
 | : | | : | | : : | : |  
 Db 8089 TPPPEAPAEQPKPEKPAE-ETPAPAPKPEKSADQQAEEDYARRSEEEYNRL----- 8138

Qy 944 GHTQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSAIDLKTSVVDLLYWRD---I 1000  
 || : || || | : | : | | : : | | :  
 Db 8139 --TQQQ-----PPK-----AEKPAPAPAPKPEQPAPAPKSRGLATKKKLNLAELIELL 8186

Qy 1001 KKTGV-----VFGASLFLLLS 1016  
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 Db 8187 KKLGLEPGLEKAGAGLGNLLS 8207

RESULT 11

US-09-976-594-726

; Sequence 726, Application US/09976594

; Patent No. 6673549

; GENERAL INFORMATION:

; APPLICANT: Furness, Michael

; APPLICANT: Buchbinder, Jenny

; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS

; FILE REFERENCE: PA-0041 US

; CURRENT APPLICATION NUMBER: US/09/976,594

; CURRENT FILING DATE: 2001-10-12

; PRIOR APPLICATION NUMBER: 60/240,409

; PRIOR FILING DATE: 2000-10-12

; NUMBER OF SEQ ID NOS: 1143

; SOFTWARE: PERL Program

; SEQ ID NO 726

; LENGTH: 2468

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc\_feature

; OTHER INFORMATION: Incyte ID No. 6673549 4295277CD1

US-09-976-594-726

Query Match 5.0%; Score 296.5; DB 4; Length 2468;

Best Local Similarity 21.5%; Pred. No. 2.5e-09;

Matches 264; Conservative 148; Mismatches 459; Indels 355; Gaps 59;

Qy 2 EDLDQSPLVSSS-DSPPRQPAPFKYQ---FVREP-----EDEE 35  
 || :: ||:| || : : | : ::|| | |:  
 Db 956 EDGEHVCVSASKHSPTEDDEESAKAEADAYIREKRESVASGDDRAEEDMDEAIEKGEAEQ 1015

Qy 36 EEEEEEEDEDEDLEEEV-LERKPAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPL 94  
 ||| :||: || | | | : | | | | | : | | |  
 Db 1016 SEEEADEEDKAEDAREEEYEPEKMEAEYVMAVVDKAAEAGGAEQYGFLLTPTKQLG-- 1073

Qy 95 PAAPPVAPERQPSWDPSVSPVSPAPSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQ 154  
 : | | : | : | : | | | | : | | | : | :  
 Db 1074 ----AQSPGREPA--SSIHDETLPGGSESEATA-----SDEENREDQPEEFTATSGYT 1120

Qy 155 AEPVWTPAPAPAAPSTPAAPKRRGSSGAVVXXXXKIMDLKEQPGNTISAGQE-----D 209  
 : | | ||| : | : | | ||  
 Db 1121 QSTIEISSEPTPMDEMSTP-----RDVMSDETNNEETESPSQEFVNITK 1164

Qy 210 FPSVLLETAASXPS-LSPLSAASFKE-----HEYLGNLSTVLPTEGTLQENVSEAS 259  
 : | | | : : : | : | : | : | : : | : :  
 Db 1165 YESSLYSQEYSKPADVTPLN--GFSEGSKTDATDGKDYNASASTISPPSSMEEDKFSRSA 1222  
  
 Qy 260 -----KEVSEKAKTLLIDRDLTEF-----SELEYSEMGs---SFS 291  
 | | | | : | | | : : | : |  
 Db 1223 LRDAYCSEV--KASTTLDIKDSISAVSSEKVSPSKSPSLSPSPSPLEKTPLGERSVNFS 1280  
  
 Qy 292 VSP-----KAESAVIVANPR--EEIIVKN--KDEEEKL-----VSNNILHX----- 328  
 : : | | : | : | : : : : | : : | : :  
 Db 1281 LTPNEIKVSAEAEVAPVSPPEVTQEVVEHCASPEDKTLEVVSPSQSVTGSAGHTPHYQSP 1340  
  
 Qy 329 ----QQELPTALTCLKVEDEVVSSEKAKDSFNEKRVAVEAPMREEYADFK-PFERVWEVK 383  
 | | : : | | : | : : | | : | | : | : |  
 Db 1341 TDEKSSHLPTTEV--IEKPPAVPVSEFSDAKDENERASVSPMDEPVPDESPIEKLVSPL 1398  
  
 Qy 384 DSKEDSDMLAAGGKIESNLESKVDDKKCFADSLEQTNHEKDSESSNDDTSFSTPEGIKDR 443  
 | : : | | : | | | : : | | : : | :  
 Db 1399 RS---PPLIGSESAYESFLSA--DDKASGRGAESPFEKSGKQGSQSPDQVSPVSE----- 1447  
  
 Qy 444 SGAYITCAPFNPAATESIATNIFPLLEDPTSENXTDEKK-----IEEKK-----A 488  
 : | | : : | : | | | : : : : : : :  
 Db 1448 ----MTSTSLYQDKQEGKSTDFAPIKEDFGQEKKTDDVEAMSSQPALALDERKLGDVSP 1503  
  
 Qy 489 QI-----VTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTEEVVA--N 531  
 | | : : | : : | | : | | : : | : | :  
 Db 1504 QIDVSQFGSFKEDTKMSISEGTVSDKSATP--VDEGVAEDTYSHMEGVASVSTASVATSS 1561  
  
 Qy 532 MPEGLTPDLVQACESELNEVTGKTIAYETKMDLVQTSEVMQES-LYPAAQLCP----- 584  
 | | | | : : : : : : : : | : : | : : | :  
 Db 1562 FPEPTTDD-VSPSLHAEVGSHPSTEVDDSLSVSVVQTPTTFQETEMSPSKEECPRPMSIS 1620  
  
 Qy 585 -----SFESEATPSPVLP-DIVMEAPLNSAVPSAGASVI 618  
 | | : : | | : : | : | : | :  
 Db 1621 PPDFSPKTAKSRTPVQDHRSEQSSMSIEFGQESPEQSLAMDFSRQSPDH---PTVGAGVL 1677  
  
 Qy 619 Q-----PSSSPLEASSVNYESIKHE--PENPPPY-----EEAMSVS-LKVSGIKEEIKE 664  
 | : | : | : : | | | : | : : : | :  
 Db 1678 HITENGPTEVDYSPSDMQDSSLSHKIPMEEPSYTQDNDLSELISVSQVEASPSTSSAHT 1737  
  
 Qy 665 PENINAALQETE----AP-----YISIACDLIKE---TKLSAEP-----A 697  
 | | : | | | | | : : : : | : : : :  
 Db 1738 PSQIASPLQEDTLSDVAPPRDMSLYASLTSEKVQSLEGEKLSPKSDISPLTPRESSPLYS 1797  
  
 Qy 698 PDFSDYSEMAKVEQVPDPHSELVEDSSPDSEPVDLFS----- 734  
 | | | : | : | | | | : | |  
 Db 1798 PTFSDSTSAVK-EKTATCHS----SSSP---PIDAASAEPYGFRAVLFDTMQHHLLALNR 1849  
  
 Qy 735 DDSIPDVP-----QKQDETVMVLVKESLTETSFESMIEYENKEKLSALPPE 779  
 | | | : | : | | | : | : | : | :  
 Db 1850 DLSTPGLEKDSGGKTPGDFSYAYQKPEET-----TRSPDEEDYDYESYEKTTTSDV 1901  
  
 Qy 780 GGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFISKEAQIR 839  
 | | | : : : | : | | | | : | : | :  
 Db 1902 GGY-YYEKIERTTKSPSDSGYSYE--TIGKTTKTP-----EDGDYSYE--IEKTTTRTP 1950

Qy 840 ETETFS DSSPIEIIDEFP TLISSKTDS---FSKLAREYTDLEVSHKSEIANAPDGAGSLP 896  
 | :| || || | : | | : :| | :  
 Db 1951 EEGGYSYD-----ISEKTTSPPEVSGYSYEKTERSRRLLDDISNGYDDS---- 1994

Qy 897 CTELP HDLSLKNIQPKVEEKISFSDDFSKNGSATS KVL LPPDV SALGHTQAE-IESIVK 955  
 : | | : : ||| : : || || | : || | :  
 Db 1995 -EDGGHTLGDP SYSYETTEKITSFPES EGYSETSTKTT RTPDTSTYCYETA EKITRTPQ 2053

Qy 956 PKVLEKE-----AEKKLP SDTEKE 974  
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 Db 2054 ASTYSYETSDLCYTAEKKSPSEARQD 2079

RESULT 12

US-09-149-476-411

; Sequence 411, Application US/09149476  
 ; Patent No. 6420526  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rosen et al.  
 ; TITLE OF INVENTION: 186 Human Secreted proteins  
 ; FILE REFERENCE: PZ002P1  
 ; CURRENT APPLICATION NUMBER: US/09/149,476  
 ; CURRENT FILING DATE: 1998-09-08  
 ; EARLIER APPLICATION NUMBER: PCT/US98/04493  
 ; EARLIER FILING DATE: 1998-03-06  
 ; EARLIER APPLICATION NUMBER: 60/040,162  
 ; EARLIER FILING DATE: 1997-03-07  
 ; EARLIER APPLICATION NUMBER: 60/040,333  
 ; EARLIER FILING DATE: 1997-03-07  
 ; EARLIER APPLICATION NUMBER: 60/038,621  
 ; EARLIER FILING DATE: 1997-03-07  
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 ; EARLIER APPLICATION NUMBER: 60/047,600  
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 ; EARLIER APPLICATION NUMBER: 60/047,615  
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 ; EARLIER APPLICATION NUMBER: 60/047,597  
 ; EARLIER FILING DATE: 1997-05-23  
 ; EARLIER APPLICATION NUMBER: 60/047,502  
 ; EARLIER FILING DATE: 1997-05-23  
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 ; EARLIER APPLICATION NUMBER: 60/047,503  
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; EARLIER APPLICATION NUMBER: 60/047,592  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,581  
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; EARLIER APPLICATION NUMBER: 60/047,584  
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; EARLIER APPLICATION NUMBER: 60/047,587  
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; EARLIER APPLICATION NUMBER: 60/047,612  
; EARLIER FILING DATE: 1997-05-23  
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; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,601  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/043,580  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,568  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,314  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,569  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,311  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,671  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,674  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,669  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,312  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,313  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,672  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/043,315  
; EARLIER FILING DATE: 1997-04-11  
; EARLIER APPLICATION NUMBER: 60/048,974  
; EARLIER FILING DATE: 1997-06-06  
; EARLIER APPLICATION NUMBER: 60/056,886  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,877  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,889

; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,893  
; EARLIER FILING DATE: 1997-08-22  
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; EARLIER APPLICATION NUMBER: 60/056,878  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,662  
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; EARLIER APPLICATION NUMBER: 60/056,903  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,888  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,879  
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; EARLIER APPLICATION NUMBER: 60/056,894  
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; EARLIER APPLICATION NUMBER: 60/056,911  
; EARLIER FILING DATE: 1997-08-22  
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; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,845  
; EARLIER FILING DATE: 1997-08-22  
; EARLIER APPLICATION NUMBER: 60/056,892  
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; EARLIER FILING DATE: 1997-05-23  
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; EARLIER APPLICATION NUMBER: 60/047,588  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,585  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,586  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,590  
; EARLIER FILING DATE: 1997-05-23  
; EARLIER APPLICATION NUMBER: 60/047,594  
; EARLIER FILING DATE: 1997-05-23



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; EARLIER APPLICATION NUMBER: 60/047,589
; EARLIER FILING DATE: 1997-05-23
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; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/047,614
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,578
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/043,576
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/047,501
; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
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; EARLIER FILING DATE: 1997-08-22
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; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02
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Query Match          4.8%; Score 285; DB 4; Length 92;
Best Local Similarity 57.1%; Pred. No. 1.2e-10;
Matches 52; Conservative 20; Mismatches 19; Indels 0; Gaps 0;
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Qy      1079 NSALGHVNCTIKELRRLEFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVP 1138
          |:| |:| |:| :| :| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db      2 NAAMVHINRALKLIIRLFLVEDLVDLSLKLAVFMWLMTYVGAVFNGITLLILAELLIFSVP 61

Qy      1139 VIYERHQAQIDHYLGLANKNVKDAMAKIQAK 1169
          ::|:|:|:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:| |:|
Db      62 IVYEKYKTQIDHYVGIARDQTKSIVEKIPSK 92
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RESULT 13

US-08-973-462-8

; Sequence 8, Application US/08973462B  
 ; Patent No. 6191270  
 ; GENERAL INFORMATION:  
 ; APPLICANT: DRUILHE, PIERRE  
 ; APPLICANT: DAUBERSIES, PIERRE  
 ; TITLE OF INVENTION: MALARIAL PRE-ERYTHROCYTIC STAGE POLYPEPTIDE MOLECULES  
 ; FILE REFERENCE: 0660-0125-0 PCT  
 ; CURRENT APPLICATION NUMBER: US/08/973,462B  
 ; CURRENT FILING DATE: 1998-02-06  
 ; EARLIER APPLICATION NUMBER: PCT/FR96/00894  
 ; EARLIER FILING DATE: 1996-06-12  
 ; EARLIER APPLICATION NUMBER: FR 95/07007  
 ; EARLIER FILING DATE: 1995-06-13  
 ; NUMBER OF SEQ ID NOS: 29  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 8  
 ; LENGTH: 1786  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Polypeptide  
 US-08-973-462-8

Query Match 4.7%; Score 276.5; DB 3; Length 1786;  
 Best Local Similarity 20.1%; Pred. No. 2.6e-08;  
 Matches 232; Conservative 201; Mismatches 471; Indels 249; Gaps 50;

Qy	30	EPEDEEEEEEEEDEDEDLEE-----LEVLERKPAAGLSAAPVPTAPAAGAPLMDFGN	83
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Db	228	EESVEENDEESVEENVEENVEENDDGSVASSVEESIASSVDESIDSSIEENVAPTVE---	284
Qy	84	DFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAPSPLSAAVSPSKLPEDDEPPAR-	142
		:     :     :   : :         :	
Db	285	EIVAPS-----VVESVAPSVEESVEENVEESVAENVEESVAENVEESVAENVEESVAEN	338
Qy	143	----PPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRGSSGAVVXXXXKIMDLKEQ	198
		:    :      : :     : :	
Db	339	VEEIVAPTVEEIVAPTVEEIVAPSVVESVAPSVEESVEENVEESVAENVEESVAENVEES	398
Qy	199	PGNTISAGQEDFPSVLLETAAS-----XPSLSPLSAA SFKEHEYLGNLSTVLPT-EGTL	251
		: :  :   :   :  : :   : :  : :  :  :	
Db	399	VAENV---EESVAENVEESVAENVEEIVAPTVEEIVAPTVEEIVAPSVVESVAPSVEESV	455
Qy	252	QENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSVSPKAESAVI-----VANP	305
		:       :     : : :     :    :   :	
Db	456	EENVEESVAENVEESVAENVEESVAENVEESVAE-NVEESVAENVEESVAENVEESVAEN	514
Qy	306	REEIIVKNKDE-----EEKLVSNNILHX-----QQELPTALTCLKVKED-----EVV	346
		: :    :  : : : : : : : :  :	
Db	515	VEEIVAPTVEEIVAPTVEEIVAPSVVESVAPSVEESVEENVEESVAENVEESVAENVEES	574
Qy	347	SSEKAKDSFNEKRVAVEAPMREEYA-----DFKPFERVWEVKDSKEDSDMLAAGGKIESN	401
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Db	575	VAENVEESVAENVEEIVAPTVEEIVAPTVEEIVAPSVVESVAPSVEES-----VEEN	626



; Patent No. 6558903  
; GENERAL INFORMATION:  
; APPLICANT: Hodge, Martin  
; TITLE OF INVENTION: No. 6558903el Kinases and Uses Thereof  
; FILE REFERENCE: 35800/183781  
; CURRENT APPLICATION NUMBER: US/09/345,473E  
; CURRENT FILING DATE: 1999-06-30  
; NUMBER OF SEQ ID NOS: 62  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 40  
; LENGTH: 1601  
; TYPE: PRT  
; ORGANISM: C. elegans  
US-09-345-473E-40

Query Match 4.5%; Score 267.5; DB 4; Length 1601;  
Best Local Similarity 20.5%; Pred. No. 8e-08;  
Matches 229; Conservative 134; Mismatches 376; Indels 377; Gaps 56;

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Qy      29 REPEDEEEEEEEEE-----EDEDLEEEVLERKPAAGLSAAPVPTAPAAGA 76
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Qy      77 PLMDFGNDFVPPAPRGP-----LPAAPPVAPE-----RQPSWDPS-PVS--STVPAPSP 122
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Qy     123 LSA---AAVSPSK----LPEDDEPPARPPPPPPASVSPQAEPVW---TPPAPAP--AAPP 170
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Qy     171 STPAAPKRRGSSGAVVXXXXKIMDLKEQPGNTISAG-QEDFPSVLLETAASXP SLSPLSA 229
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Db      627 QTPTLAQ-----NTVPTISTDASGLVINTPASIASPSPAPS 663

Qy     230 ASFKEHEYLGNLSTVLP-----TEG-----TLQENVSEASKEVSEKAKTLLIDRDLT 276
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Db      664 AT----DVASTTAPVTPAPTPTTTTGDGAAASTTTENKEEKRSNKRKVMEILGCDES 719

Qy     277 E-----FSELEYSEMGSFSVSP-----KAESAVIVANPREEIIVK 312
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Qy     313 NKDEEE---KLVSNNILHXQQELPTALTCLVKEDEVVSSEKAKDSFNEKRVAVEAPMRE 368
      | | : :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      780 NSDGKKGVGTKLAT--VLDPNSTEPPTITAVMPKD----SSAATASNTKPKIEI----- 827

Qy     369 EYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSSESN 428
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Db      828 -----EKTPTTRDASQE-----PNNVQVTNVRKVSQESN 856

Qy     429 DDTSPSTPEGIKDRSGAYITCAPFN-----PAAT---ES 460
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Db      857 AE-SVQSIP-----RPGGIIVMSPTNQTD SAPPTGAAAKPSRFQVTKSADPIATPISSS 910

Qy     461 IAT-NIFPLLEDPTSENXTDEKKIEEK-KAQIVTEKNTSTKTSNPFFVAAQDSETDYVTT 518
      |:| :||: | | | | | :| ||:| | :| :| :| :| :| :|
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Db 911 ISTATVIPIVA-ATPTNITSEPVIVQPIAQQVITHLATPSPVSHSL---SSNSSPSATTH 966  
 Qy 519 DNLTKVTEEVVANMP-EGLTPDLVQACESELNEVTGTKIAYETKMDLVQTSEVMQESLY 577  
 |:: : : :| | | :| | :| |  
 Db 967 SNMSSI--QSTTSVPGRRTVQPVSA-ESGISSSISTPHPEPT----- 1007  
 Qy 578 PAAQLCPSFEESEATPSPVLPDIVMEAPLNSAV-----PSAGASVIQSSSPLEASSVNY 632  
 || || | :| :| || | || : | ||:  
 Db 1008 PAITSCP-----PPVPSVPPVVSNGTLNLEVAPKQTPSATNQNVDTQHSSSTASTATL 1060  
 Qy 633 ESIKHEPEN-----PPPYEEAMSVS-----LKVSGIKEEIKEPENINAA 671  
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 Db 1061 --VSETPATVHVTPISVPAPVQEPLVIDHHSVDLTQLDSELRKVSGVSHS-ASPSTVVES 1117  
 Qy 672 LQETEAPYISIIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELVEDSSPDSEPVD 731  
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 Db 1118 LTSMTPTQTIPLACQTV-PASIGQAPAVIAAAHA-----AS 1151  
 Qy 732 LFSDDSIIPDVPQKQDETVMVLVKESLTETSFESMIEYENKEKLSALPPEGKPYLESFKLS 791  
 | :| :| | :| || : ||| || | :  
 Db 1152 LIPNASVPQSPSRLD-----AETGLAGL-----HEKLEAL-----KME 1184  
 Qy 792 LDNTKDTLLPDE---VSTLSKKEKIPLQ-----MEELSTAVYSNDDLFIKSEAQIRET-- 841  
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 Db 1185 QDRRED--MGDDAIGTTTTDGKDEIPIDTLKGLAEALGKVIHADG-----RETTT 1232  
 Qy 842 -----ETFSDDSPIEII-----DEFPTLISSKTDSEFSKLAREYTDLEVS--HKSEIANAP 889  
 :|| :| | :| :| | | | | : :|  
 Db 1233 MPPDHPDLTDASTQQLISPSNPDLTTMSSAVEGSASSTMIEDIDASTSAVDASMMNSMP 1292  
 Qy 890 DGAGSLPCTELPHDLKNIQPKVEEKISFSDDFSNGSATSQVLLLPDVSALGHTQAE 949  
 || :| : :| | | | : :| |  
 Db 1293 PGA-----QNSTDQIPAAMTSLMDQECAQSMTSSITR-----NTTGTKLAT 1333  
 Qy 950 IESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSAD 985  
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 Db 1334 FENL-----ETALSSTLGTHIRQPNAPSSRD 1359

RESULT 15

US-08-978-277A-4

; Sequence 4, Application US/08978277A

; Patent No. 6582956

; GENERAL INFORMATION:

; APPLICANT: Gelman, Irwin H.

; TITLE OF INVENTION: TUMOR SUPPRESSOR GENE

; NUMBER OF SEQUENCES: 20

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond

; STREET: 30 Rockefeller Plaza

; CITY: New York

; STATE: NY

; COUNTRY: USA

; ZIP: 10112-0228

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

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;   OPERATING SYSTEM:  DOS
;   SOFTWARE:  FastSEQ Version 1.5
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/978,277A
;   FILING DATE:
;   CLASSIFICATION:  514
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  08/665,401
;   FILING DATE:  18-JUN-1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Clark, Richard S
;   REGISTRATION NUMBER:  26,154
;   REFERENCE/DOCKET NUMBER:  A30558 - 165/34008
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  212-408-2558
;   TELEFAX:  212-765-2519
;   TELEX:
;   INFORMATION FOR SEQ ID NO:  4:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  1596 amino acids
;   TYPE:  amino acid
;   STRANDEDNESS:  single
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  peptide
;   HYPOTHETICAL:  NO
;   ANTI-SENSE:  NO
;   FRAGMENT TYPE:  internal
;   ORIGINAL SOURCE:
US-08-978-277A-4

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Query Match          4.5%;  Score 265;  DB 4;  Length 1596;
Best Local Similarity 21.3%;  Pred. No. 1.1e-07;
Matches 232;  Conservative 145;  Mismatches 422;  Indels 288;  Gaps 47;

```

```

Qy      2 EDLD--QSPLVSSSDSPPRQPAPFKYQFVREPEDE-----EEEEEEEEDEDEDLEELEV 54
      |:|:  :|  :||:|  |  :|  ||:  ||  :  :  |
Db      620 EELEKVKSATLSSTDST-----VSEMQDEVKTVGEEQKPEEPKRRVDTSVSWEA 668

Qy      55 LERKPAAGLSAAPVPTAPAAGAPL-----MDFGNDFVPPAPR----- 91
      |  ::  |  ::  |  |  :  |  ||  ||  :  :
Db      669 LICVGSSKKRARKASSSDDEGGPRTLGGDSHRAEEASKDKEAGTDAVPASTQEQDQAQGS 728

Qy      92 -GPLPAAPPVAPERQPSWDPSVSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPPAS 150
      |  ||  |  |  :|:  |  :|  |  ||  |  |  :
Db      729 SSPEPAGSPSEGEVSTWE-----SFKRLVTPRKK---SKSKLEEKAEDESS--VEQLSTE 778

Qy      151 VSPQAEPVWTPPAPAPAAPPSTPAAPKRRGSSGAVVXXXXKIMDLKEQPGNTISAG---- 206
      :  |  |  |  :  |  |  |  |  |  |  |  |  :|
Db      779 IEPSREESWV-----SIKKFIPGRRKKRA-----DGKQEQATVEDSGPVEI 819

Qy      207 QEDFPSVLLETAASXPSLSPLSAAAFKEHEYL---GN-----LSTVLPTEGTLQENVSE 257
      ||  |:|  ||:  ||  :  |  |  :  ||  |  |  :|  |
Db      820 NEDDPNV-----PAVVPLSEYNAVEREKMEAQGNTELPQLLGAVYVSE-----E 863

Qy      258 ASKEVSEKAKTLLID--RDLTEFSELEYSEMGSFSVSPKAESAVIVANPREEIIVKNKD 315
      ||  :  :||  |  :|  |  |  :  :|  :  |  |  ||:  |
Db      864 LSKTLVHTVSVAVIDGTRAVTSVEERSPSWISASVT-EPLEHTAGEAMPPVEEVTEKDII 922

```

Qy 316 EEEKLVSNILHXQQELPTALTCLVKE-----DEVVSSEKAKDSFNEKRVAVEAPMREEY 370  
 || | | : : | | : : || | |  
 Db 923 AEETPV-----LTQTLPEGKDAHDDMTSEVDFTS-----EAVTATET 960

Qy 371 ADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSSESSNDD 430  
 : : | | : : | : : : : : : : : : : : :  
 Db 961 SEALRTEEVTEASGAETTDMVSAVSQLTDS-----PDTTEEATPVQEVESGVLD 1010

Qy 431 TS-----FPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSSENXTDEK 481  
 | : : : : | | : : | : : :  
 Db 1011 TEEERQTQAILQAVADKVKEES-----QVPATQTVQRTGSKALE-----KVE 1053

Qy 482 KIEEKKAQIVTEKNTSTKTSNPFVFA-----AQDSETDYVTTDNLTKVTEEVVANMPEGL 536  
 : : || : : || | | | | | | | | | |  
 Db 1054 EVEEDSEVLASEKEKDVMPKGPVQEAHLAQGSETQAT-----PESL 1098

Qy 537 TPDLVQEACESELNEVTGTKIAYETKMDLVQTSVMQESLYPAAQLCPSFEESEATPSPV 596  
 | : || : : : : : : : : : : : :  
 Db 1099 -----EVPEVT-ADVDHVATCQVIKLQQLMEQAVAPES--ETLTDSETNGSTP 1144

Qy 597 LPD-----IVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYEEAMS 650  
 | | : : | | : | : : | : : | | | |  
 Db 1145 LADSDTADGTQQDETIDSQDSKATAAVRQSQVTEEEAATAQKEEPSTLPNNVPAQE---- 1200

Qy 651 VSLKVSIGIKEEIKPENINAAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVE 710  
 | : || | : | : : | : : : : | : | |  
 Db 1201 -----EHGEEPG--RDVLEPTQQELTAAAVPVLAKTEVGQEGEVDWLD-GEKVKEE 1248

Qy 711 QPVPDHSELVEDSSPDSE-PVDLFSDDSDIPDVPQKQD-ETVMLVKESLTETSFESMIEYE 768  
 | | | | | : : | : | : | : : : | | | : : |  
 Db 1249 QEVFVH-----SGPNSQKAADVTDSEVMGVAGCQEKESTEVQSLSLEEEMETDVEKE 1302

Qy 769 NKE-KLSALPPEG-----GKPYLESFKLSLDNTK-----DTLLPDEVSTL 807  
 : | | : | | | | | : | | :  
 Db 1303 KRETKPEQVSEEGEQETAAPHEGTYGKPVLTLDMPSSSERGKALGSLGGSPSLPDQ----- 1358

Qy 808 SKKEKIPLQMEELSTAVYSNDDLFIKSEAQIRETETFSDS--SPIEIDE--FPTLISSK 863  
 | | | : : | | : : || | : : || | : | |  
 Db 1359 DKAGCIEVQVQSLDTTVTQTAEAV----EKVIETVVISETGESPECVGAHLLPAEKSSA 1413

Qy 864 TDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFS--- 920  
 | | : : : : | : | | : | : : : || |  
 Db 1414 TGGHWTLQHAEDTVPLGPESQ-----AESIPIIVTPAPES--TLHPDLQGEISASQRE 1464

Qy 921 -----DDFSKNGSATSQVLLLPDVSALGHTQAEIESIVKPKVLEKEAEKKLP 968  
 | | : | || | : : | : | : : : | :  
 Db 1465 RSEEDKPDAGPDADGKESTAIEKVLKAEPEILELESKSNKIVLNVIQTAVDQFARTETA 1524

Qy 969. SDTEKED 975  
 : | |  
 Db 1525 PETHAYD 1531

Search completed: September 29, 2004, 18:21:04  
 Job time : 33.2441 secs

OM protein - protein search, using sw model

Run on: September 29, 2004, 18:05:43 ; Search time 28.8322 Seconds  
 (without alignments)  
 3930.111 Million cell updates/sec

Title: US-09-830-972-29  
 Perfect score: 5923  
 Sequence: 1 MEDLDQSPLVSSSDSPRPQ.....VKDAMAKIQAKIPGLKRKAE 1178

Scoring table: BLOSUM62  
 Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0  
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
 Maximum Match 100%  
 Listing first 45 summaries

Database : PIR 78:\*  
 1: pir1:\*  
 2: pir2:\*  
 3: pir3:\*  
 4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

		%					
Result		Query					
No.	Score	Match	Length	DB	ID	Description	
1	787.5	13.3	776	2	A46583	neuroendocrine-spe	
2	688	11.6	208	2	I60904	neuroendocrine-spe	
3	671	11.3	267	2	A60021	tropomyosin-relate	
4	528	8.9	2484	2	T26216	hypothetical prote	
5	519.5	8.8	2607	2	T26215	hypothetical prote	
6	340.5	5.7	222	2	T26213	hypothetical prote	
7	331	5.6	7962	2	I38346	elastic titin - hu	
8	325.5	5.5	5327	2	T13564	microtubule-associ	
9	324.5	5.5	865	2	A47282	calcium-binding pr	
10	320.5	5.4	873	2	A47283	calphotin - fruit	
11	299.5	5.1	3488	2	T34418	hypothetical prote	
12	299	5.0	3924	2	S37431	ankyrin 2, neurona	
13	290.5	4.9	1274	2	T16251	hypothetical prote	



14	289	4.9	2364	2	A56577	microtubule-associ
15	289	4.9	2464	1	QRMSPL	microtubule-associ
16	287.5	4.9	971	2	T19431	hypothetical prote
17	285.5	4.8	1621	2	A82255	hypothetical prote
18	278	4.7	1948	2	S00485	gene 11-1 protein
19	274	4.6	3507	2	T34513	hypothetical prote
20	272.5	4.6	1829	2	T24583	hypothetical prote
21	272.5	4.6	2361	2	T25752	hypothetical prote
22	271	4.6	2187	2	T30826	nascent polypeptid
23	270	4.6	1230	2	T22458	hypothetical prote
24	267.5	4.5	1851	2	T19964	hypothetical prote
25	263.5	4.4	2409	1	A60979	versican precursor
26	262.5	4.4	6642	2	T29757	protein UNC-89 - C
27	261	4.4	1558	2	B71603	RESA-H3 antigen PF
28	260.5	4.4	3381	2	T42389	versican precursor
29	259.5	4.4	1828	2	A40115	microtubule-associ
30	258	4.4	1616	2	G64242	cytadherence-acces
31	257.5	4.3	5170	2	T15348	hypothetical prote
32	256	4.3	990	2	I51618	nucleolar phosphop
33	256	4.3	1634	2	T26517	hypothetical prote
34	255.5	4.3	1684	2	JW0057	gravin - human
35	253	4.3	1189	2	S56852	hypothetical prote
36	252.5	4.3	1224	2	T14007	microtubule-associ
37	252	4.3	4377	2	A55575	ankyrin 3, long sp
38	250.5	4.2	1824	1	QRHUMT	microtubule-associ
39	250.5	4.2	1830	2	A37981	microtubule-associ
40	248	4.2	1825	2	S13507	microtubule-associ
41	248	4.2	1890	2	T04556	hypothetical prote
42	248	4.2	3421	1	WZBEB6	367K tegument prot
43	246	4.2	1110	2	I51116	NF-180 - sea lampr
44	244.5	4.1	1029	2	T30351	mucin-like protein
45	243	4.1	1320	2	JC5630	TCOF1 protein - mo

#### ALIGNMENTS

##### RESULT 1

A46583

neuroendocrine-specific protein, splice form A - human

N;Contains: neuroendocrine-specific protein, splice form B

C;Species: Homo sapiens (man)

C;Date: 24-May-1996 #sequence\_revision 24-May-1996 #text\_change 05-Nov-1999

C;Accession: A46583; I60903

R;Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; Van de Ven, W.J.

J. Biol. Chem. 268, 13439-13447, 1993

A;Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-specific gene and identification of its 135-kDa translational product.

A;Reference number: A46583; MUID:93293865; PMID:7685762

A;Accession: A46583

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-776 <ROE1>

A;Cross-references: GB:L10333; NID:g307306; PIDN:AAA59950.1; PID:g307307

A;Accession: I60903

A;Status: preliminary; translated from GB/EMBL/DDBJ  
A;Molecule type: mRNA  
A;Residues: 421-776 <ROE2>  
A;Cross-references: GB:L10334; NID:g307308; PIDN:AAA59951.1; PID:g307309  
C;Genetics:  
A;Gene: GDB:RTN1; NSP  
A;Cross-references: GDB:203968; OMIM:600865  
A;Map position: 14q21-14q22

Query Match 13.3%; Score 787.5; DB 2; Length 776;  
Best Local Similarity 31.9%; Pred. No. 3.1e-25;  
Matches 229; Conservative 91; Mismatches 190; Indels 207; Gaps 25;

```

Qy      588 ESEATPSPVLPDI--VMEAPLNSA-----VPSAGASVIQPSSSPLE---ASSVNY---- 632
      |  ||| |||:  :  | |:      |:  | :  : ||:  | :  |
Db      141 EELGTPGPSLPDVPGIESRGLFSSDSGIEMTPAESTEVNKILADPLDQMKAEAYKYIDIT 200

Qy      633 --ESIKHEPENPPPYEEA-----MSVSLKVSGIKEEIKEPENINAAL-----QET 675
      | :||: :: | |:      :||| |::| || :  :  : |
Db      201 RPREEVKHQEQHHPELEDKDLDFKNKDTDISIKPEGVREPDK-PAPVEGKIIKDHLLEEST 259

Qy      676 EAPYISIIACDL-----IKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELVED 722
      ||||  ||      :| |  ||::      :: | :  ::
Db      260 FAPYID---DLSEEQRRAPQITTPVKITLTEIEPSVE-----TTTQEKTPKQDICK 309

Qy      723 SSPDSEPVDLFS---DDS-----IPDVPQKQ-----DETVMLVKESLTETSF 761
      |||: |  | ||      | : |      || :  :||:
Db      310 PSPDTVPTVTVSEPEDDSPGSITPPSSGTEPSAAESQGKGSISEDELITAIKEA----- 363

Qy      762 ESMIEYENKEKLSALPPEGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELS 821
      : || |  :  :|      || |  || :  :
Db      364 -KGLSYETAENPRPVGQLADRP-----EVKARSGPPTIPSPLDHEA 403

Qy      822 TAVYSNDDLFIKSEAQIRETETFSDSPIEIIIDFP---TLISSKTDSEFS----- 868
      :: | |      | ||:: | |      : |  ||
Db      404 SSAESGD-----SEIELVSEDPMMAEDALPSGYVSFGHVGGPPPPSP 444

Qy      869 -----KLAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSD 921
      : || : |: : | :  : |      : || |  || |
Db      445 ASPSIQYSILREEREAEELDELIIESCDASSAS-----EESPKREQDSPPMKPSALD 496

Qy      922 DF-----SKNGSATSKVLL-----LPPDVSA LGHTQAEIESIVKP 956
      | : | |  |      |||  ||  | :  : |
Db      497 AIREETGVRAEERAPSRRGLAEPGSFLDYPSTEPQPGPELPPGDGAL-----EPETPMLP 551

Qy      957 KVLEKEAEKKLPSDTEKEDRSPSA-----IFSADLGKTSVVDLLYWRDIK 1001
      : | :  :||:|      :|  | |  :||| ||||
Db      552 -----RKPEEDSSSNQSPAATKGPGLPGAPPPLLF---LNKQKAIDL YWRDIK 599

Qy      1002 KTG VVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRA 1061
      :||: |||: | || ||| ||: ||| || ||||| ||| :||: ||: ||||| :|
Db      600 QTGIVFGSFLLLFLSLTQFSVVSVVAYLALAALSATISFRIYKSVLQAVQKTDEGHPFKA 659

Qy      1062 YLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALF 1121
      ||| | : :||: :|||: :|| | :||| ||||| ||||| : |||||
Db      660 YLELEITLSQEIQKYTDCLQFYVNSTLKELRRLFLVQDLVDLSLKFAVLMWLLTYVGALF 719

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QY 1122 NGLTLILALISLFSVPVIYERHQAIIDHYLG LANKNVKDAMAKIQAKIPGLKRKAE 1178  
|||:::||:||||: ||| :||| | ||| :: :||| || |  
Db 720 NGLTLLIMAVVSMETLPVVVKHQAOIDOYLGLVRTHINAVVAKIQAKIPGAKRHAE 776

I60904

neuroendocrine-specific protein C - human

C;Species: Homo sapiens (man)

C;Date: 24-May-1996 #sequence revision 24-May-1996 #text change 05-Nov-1999

C;Accession: I60904

R; Roebroek, A.J.; van de Velde, H.J.; Van Bokhoven, A.; Broers, J.L.; Ramaekers, F.C.; Van de Ven, W.J.

J. Biol. Chem. 268, 13439-13447, 1993

A;Title: Cloning and expression of alternative transcripts of a novel neuroendocrine-specific gene and identification of its 135-kDa translational product.

A:Reference number: A46583; MUID:93293865; PMID:7685762

A;Accession: I60904

A:Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: mRNA

A;Residues: 1-208 <RES>

A;Cross-references: GB:L10335; NID:g307310; PIDN:AAA59952.1; PID:g307311

C; Genetics:

A;Gene: GDB:RTN1; NSP

A:Cross-references: GDB:203968; OMIM:600865

A;Map position: 14q21-14q22

Query Match 11.6%; Score 688; DB 2; Length 208;  
Best Local Similarity 67.5%; Pred. No. 6.2e-22;  
Matches 129; Conservative 32; Mismatches 30; Indels 0; Gaps 0;

Qy           988 KTSVVDLLYWRDIKKTGVVFASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVI 1047  
             | : | : |||||::||: | | | : | | : | | | : | | | : | :

Db 18 KSOAIDLLYWRDIKOTGIVFGSFLLLFSLTQFSVVSVVAYLALAALSATISFRIYKSVL 77

**Qy**            1048 QAIQKSDGHPHFRAYLSEVAISEELVQKYSNSALGHVNCTIKELRRRLFLVDLDLSLKLF 1107  
|||:::|||::||| : ::| : ||:: : | : |||::| :

Db 78 QAVQKTDEGHPPFKAYLELEITLSQEQIQKYTDCLQFYVNSTLKELRRLFLVQDLVDSLKF 137

```
QY      1108 AVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLG LANKNVKDAMAKIQ 1167  
          ||||| : | ||||||| ::::: |:| : ||||| |||   ::    :|||
```

Db 138 AVLWLLTYVGALFNGLTLLMAVVSMFTLPVVYVKHQAQIDQYLGLVRTHINAVVAKIQ 197

Qy 1168 AKIPGLKRKAE 1178

\_\_\_\_\_

Db 198 AKIPGAKRHAEE 208

### RESULT 3

A60021

tropomyosin-related protein, neuronal - rat

C;Species: Rattus norvegicus (Norway rat)

C;Date: 03-Mar-1993 #sequence revision 03-Mar-1993 #text change 05-Nov-1999

C;Accession: A60021

R;Wieczorek, D.F.; Hughes, S.R.

Brain Res. Mol. Brain Res. 10, 33-41, 1991

A;Title: Developmentally regulated cDNA expressed exclusively in neural tissue.  
A;Reference number: A60021; MUID:91278684; PMID:1647480  
A;Accession: A60021  
A;Molecule type: mRNA  
A;Residues: 1-267 <WIE>  
A;Cross-references: EMBL:X52817; NID:g456549; PIDN:CAA37001.1; PID:g456550  
C;Comment: This neuronal-specific mRNA was identified by hybridization to an  
alpha-tropomyosin probe but does not show homology in amino acid sequence.

RESULT 4

hypothetical protein W06A7.3c - *Caenorhabditis elegans*

C:\Date: 15-Oct-1999 #sequence revision 15-Oct-1999 #text change 15-Oct-1999

R;Ainscough, R.

A;Reference number: Z20173

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Residues: 1-2484 <WIL>

A;Experimental source: clone W06A7

A; Gene: CESP:W06A7.3c

A; Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2339/2; 2463/2

```

QY      1 MEDLDQSPLVSSSDSPRPQPAFKYQFVREPEDEEE-----EE 38
      :| :: |      | : ||      |   | :| | :      :|
Db    1397 LEKVEVQP--DLSQNSPAPHKIIDLHF-NIPKDHEDYGNDYVPFGTESSEESQKADGNQE 1453

```

Qy	39	EEEEED-----EDEDLEELVLERKPA-----AGLSAAP-----	67
Db	1454	NQEEEDVVAELNFHPIRQWRDEDVISLQSLKSLVAEVCITDVDASDVNEQDEESTLKIL	1513
Qy	68	--VPTAPAAGAPLMDFGNDVFPPAPRGPLPAAPPVAP--ERQPSW-----	108
Db	1514	KVVPSEPSLLE--LDFTND--PKVIHVPIPLMEPATMYLEEMVEWIIADAVKEVSEMEVV	1569
Qy	109	-----DPSPVSSSTVPAPSPLSAAAVSPSKLP-EDDEPPARPPPPPPASVSPQAEPVW	159
Db	1570	TESEISEMAPQVSESTCPIPEPL-----ADLKLPEVDEDEKTPEPEPVVPGQVQERIIP	1624
Qy	160	TPPAPA-PAAPPSTPAAPKRRGSSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVL--LE	216
Db	1625	VEQAPTIPQRPPRAP-----KSELPKVAKPLD	1651
Qy	217	TAASXPSLSPLSA-----ASFKEHEYLGNLSTVLPTTEGTLQENVSEASKEVSEKAKTLL	270
Db	1652	DSKSRVRFAPLNIKLGRTYSEEQQKELVESLERPL-TIITQQKPPEKPTEDIG--ALSPL	1708
Qy	271	IDRDLTEFSELEYSEMGSFSVSPKAESAVIVANPREEIIIVKNKDEEEKLVSNNILHXQQ	330
Db	1709	SPNTLAEYEEVPMMDMQS-----VPHSPQE-----KQEEIEALSEII-----	1745
Qy	331	ELPTALTCLKVKEDEVVSSEKAKDSFNEKRVAVEAPMREEYADFK---PFERVWEVKDSKE	387
Db	1746	EEPQAMKEVEKPVE-SAPEKD NESLEAPEI-INEPIRRVLVETKIMGPGKSLNEDNDDDD	1803
Qy	388	D-SDMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSSESS---NDDTSFPSTPEGIKD	442
Db	1804	DGSECLDSIGDLS---ERTIQR--FNTSIDDPSIRRDSFSSISSFGDRQKFRTAIENIRQ	1858
Qy	443	RSGAYITCAPFNPAATESIATNIFPLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSN	502
Db	1859	-----DLLPFQSSVSQYLRSSPNP-----SQQLLVTN-----	1885
Qy	503	PFFVAAQDSETDYVTTDNLTKVTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETK	562
Db	1886	----LSMDSPSD--LSPNAPPVGFENTAQFLEKLQQE-DRPSAEGSIDSSGFEEKVDHE--	1936
Qy	563	MDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLDPDIMEAPLNSAVPSAGASVIQPSS	622
Db	1937	-----GLDEFAAPP-----VHDPMQKSVFGSLGSDDMKPGS	1967
Qy	623	SP-----LEASSVNYESIKHEPENPPPYEEAMSVSLKVSGIKEEIKEPENIN-----AAL	672
Db	1968	QDDGFVFIERNEAN-----EATLKNQKMSSHNDVIEKNYFNDNAPTAAL	2013
Qy	673	QETEAPYISIACDLIKETKLSAEPAPDFSDYSEMA-----KVEQPVDPHSEL	719
Db	2014	--LESPIAEEARKLVQDAVESAE-----SEYKKQAVDSGDEIGRELLDNVEQKIEQVKEP	2065
Qy	720	VEDSSPDSEPVDLFSDDSI PDVPQKQDETVMVLKESLTETSFSMIEYENKEKLSALPPE	779
Db	2066	IVDSL--HKAYDGVGVFVHETV PNAVDVDFVREAEKQLPESPVEKIE-----TPE	2113

Qy 780 GGKPYLESFKLSLDNTKDTL--LPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFISKEAQ 837  
 | : || : ||| : : | | | : | :  
 Db 2114 -----PLVDIHDTVDKVHDEVDFNFLRREPTP-PFETDDVAPLSDDKPQFGNQTP 2161

Qy 838 IRETETFSOSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPC 897  
 : || : | : | : : : : : : | | :  
 Db 2162 EEDETTFDRKGPLTIPEEVEKAAAAQNNDLD----DFDPLVTSNTGAAFGAAGVAAAA-- 2215

Qy 898 TELPHDLSLKNIQPKVEEKISFSDDFSNGSATSQVLLLPDVSALGHTQAEIESIVKPK 957  
 : : || : : : : : : : : : :  
 Db 2216 -----VESLTEEEM-----FGH--QKFETVPRPP 2237

Qy 958 VLEKEAEKKLPSTEKEDRSPSAIFSADLG-----KT-- 989  
 | | || || : : || : :  
 Db 2238 T-----PPKDISDEDVKPSTV---NLGPSHHSHSPSSPHHSILKHHGDAWIDFKTVP 2286

Qy 990 -SVVDLLYWRDIKKTGVVFGASLFLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIO 1048  
 | : : : || || || : : | : : : | | | : : : |  
 Db 2287 PCVLDVIYWRDAKSAIVLSLALLVFLVLAQYPLLTVTYSLLLALGAAAGFRVFKKVEA 2346

Qy 1049 AIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFA 1108  
 | : : | || | : : : : | : : : | | : : : | : : : :  
 Db 2347 QIKKTDSEHPFSEILAQDLTLQEKVHAQADVFEHATCIANKLKKLVFVESPLESIKFG 2406

Qy 1109 VLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQA 1168  
 : : : | || : : | || || : : || : : | | : : : |  
 Db 2407 LVLWSLTYYIASWFSGFTLAILGLLVGVFVSPKVEYNQEAIDPHLATISGHLKNVQNIIDE 2466

Qy 1169 KIPGLK 1174  
 | : | :  
 Db 2467 KLPFLR 2472

# RESULT 5

T26215

hypothetical protein W06A7.3a - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C;Accession: T26215

R;Ainscough, R.

submitted to the EMBL Data Library, August 1996

A;Reference number: Z20173

A;Accession: T26215

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-2607 <WIL>

A;Cross-references: EMBL:Z78066; PIDN:CAB01522.2; GSPDB:GN00023; CESP:W06A7.3a

A;Experimental source: clone W06A7

C;Genetics:

A;Gene: CESP:W06A7.3a

A;Map position: 5

A;Introns: 1827/1; 1866/3; 1963/3; 1990/3; 2262/1; 2289/1; 2412/1; 2462/2;

2586/2

Query Match 8.8%; Score 519.5; DB 2; Length 2607;  
 Best Local Similarity 20.4%; Pred. No. 1.8e-13;  
 Matches 292; Conservative 175; Mismatches 474; Indels 491; Gaps 55;

Qy	1	MEDLDQSPLVSSDSPRPQPAFKYQFVREPEDEEE-----EE	38
Db	1397	LEKVEVQP--DLSQNSPAPHKIIDLHF-NIPKDHEDYGNDYVPFGTESSEESQKADGNQE	1453
Qy	39	EEEEED-----EDEDLEELEVLERKPA-----AGLSAAP-----	67
Db	1454	NQEEEDVVAELNFHPIRQWRDEDVISLQSLKSLVAEVCITDVDASDVNEQDEESTLKIL	1513
Qy	68	--VPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAP--ERQPSW-----	108
Db	1514	KVVPSEPSLLE--LDFTND--PKVIHVPIPLMEPATMYLEEMVEWIIADAVKEVSEMEVV	1569
Qy	109	-----DPSPVSSTVPAPSPLSAAAVSPSKLP-EDDEPPARPPPPPPASVSPQAEPVW	159
Db	1570	TESEISEMAPQVSESTCPIPEPL-----ADLKLPVEDDEKTPEPEPVVPGQVQERIIP	1624
Qy	160	TPPAPA-PAAPPSTP-----AAPKRRGSSGAVVXXXXKIMDLKEQPGNTISAGQE---	208
Db	1625	VEQAPTIPQRPPRAPKSELPKVAKPLDDSKS-----RVRFAPLNIKLGRITYSEEQQKEL	1678
Qy	209	----DFPSVLLETAASXP-----SLSPLSAASFKEHEY--LGNLSTVLPTTEGLQEN	254
Db	1679	VESLERPLTII-TQQKPPEKPTEDIGALSPLSPNTLAEYEEVPMMDMQSVPHSPQEKQEE	1737
Qy	255	VSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSVSPKAESAVIVANPREEIIVK--	312
Db	1738	I-EALSEIIEEPQAM-----KEVEKPVESAPEKDNESLEAPEIINEPIRRVLVETK	1787
Qy	313	-----NKDEEEKLVSNNILHXQQELPTALTCLKVEDEVVSSEKAKDSFNEKRVAVEA	364
Db	1788	IMGPGKSLNEDNDDDDDGSECLDSIGDL-----SERTIQRFN--TSIDD	1829
Qy	365	P--MREEYADFKPFERVWEVKDSKED--SDMLAAGGKIESNLESKVDKKCFADSLEQTNH	420
Db	1830	PSIRRDSFSSISSFGDRQKFRTAIENIRQDLLPFQSSVSQYLRSSPNP---SQQLLVTNL	1886
Qy	421	EKDSESSNDDTSFPSTPEGI-----KDRSGA--YITCAPFNPAATESIATNIF	466
Db	1887	SMDSPS---DLSPNAPPVGFENTAQFLEKLQQEDRPSAEGSIDSSGFVKVDHEGLDEF	1943
Qy	467	PLEDPTSEN-----XTDEKK-----IEEKKAQIVTEKNTSTKTSNPFVAAQDS	511
Db	1944	PPVHDPMQKSVFGSLGSDDMKPGSQDDGFVFIERNEANEATLKKNQKMSHHNDVIEKNY	2003
Qy	512	ETDYVTTDNLTKVTEEVVANMPEGLTPDLVQEACESELNEV-TGTKIAYE---TKMDLV	566
Db	2004	FNDNAPT---AALLESPIAEARKLVQDAVESASEYKKQAVDSGDEIGRELLDNVEQKIE	2060
Qy	567	QTSEVMQESLYPAAQLCPSFEESEATPSPVLPDIMEAPLNSAVPSAGASVIQPSSSPLE	626
Db	2061	QVKEPIVDSLHKAYDGVGDFVH-ETVPNAV-DDFVREAE-----	2097
Qy	627	ASSVNYESIKHEPENPPPYEEAMSVSLKVGSIKEEIKEPENINAALQETEAPYISIACDL	686
Db	2098	-----KQLPESPVP-----EKIETPE-----PLVDIHD	2122

```

Qy      687 IK-----ETKLSAEPAPDFSDYSEMAKVEQVPDPHSELVEDSSPDSEPVDFSDSDSIPDV 741
      |      : | || | |      : | : | | : | : |
Db      2123 DKVHDEVDFNFLRREPTPFEE-----TDDVAPLSDDKPQFGNQ----- 2160

Qy      742 PQKQDETVMVLVKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLP 801
      : : || | | | | | | | | : |
Db      2161 -PEEDETTFDRKGPLT-----IP 2177

Qy      802 DEVSTLSKKEKIPLQMEELSTAVYSNDDLFIKSEAQIRETETFSDSPIEIIDEFPTLIS 861
      : ||      | : | : ||      : : | | : :
Db      2178 EEV-----EKAAAAQNND-----LDDFDPLVT 2199

Qy      862 SKT-----DSFSKLAR-----EYTDLEVSHKSEIANAPD 890
      | |      | : | : : | | | : |
Db      2200 SNTGAAGAAVGAAGAAVESLTEEEMFGHQKFETVPRPPTPPKDISDEDVK-PSTVNLGPS 2258

Qy      891 GAGSLPCTELPHD-----LSLKNIQPKVEEKIS-----FSDDFS 924
      | | : | | : | : | : | | : |
Db      2259 HHSHPSS--PHHSILKHHGDAWIDFKTVPPCAQNAFSPGEIMFLLAFFVYLSCFASFSS 2316

Qy      925 KNGSATSKVLLL-----PPDVSALG----- 944
      | : : | | : | |
Db      2317 KSLPLLDNLLSLVVYLSISLIHVKHHRKFRWNEEQATTMSKLGAVGRGLYALIAFIVNI 2376

Qy      945 --HTQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKK 1002
      : : | | | | | | | | | | | |
Db      2377 VLRVGLNVALVVGVAUSAHEAYKLTKS-----SGVLRKKEVLVDVIYWRDAKK 2423

Qy      1003 TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAY 1062
      : : | : | : | : : : | | | | | : : | | |
Db      2424 SAIVLSLALLVLFVLAKYPLLTVVVTYSLLLALGAAAGFRVFKKVEAQIKKTDSEHPFSEI 2483

Qy      1063 LESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFN 1122
      | : : : | | : : | | : : : | : : : | : : | :
Db      2484 LAQDLTLPQEKVHAQADVFEHATCIANKLKKLVFVESPLESIKFGVLVLSLTYIASWFS 2543

Qy      1123 GLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLK 1174
      | | | | | : : | | : | | : : : | | : |
Db      2544 GFTLAILGLLGVSVPKVEYNQEAIDPHLATISGHLKNVQNIIDEKLPFLR 2595

```

RESULT 6

T26213

hypothetical protein W06A7.3b - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999

C;Accession: T26213

R;Ainscough, R.

submitted to the EMBL Data Library, August 1996

A;Reference number: Z20173

A;Accession: T26213

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-222 <WIL>

A;Cross-references: EMBL:Z78066; PIDN:CAB01523.1; GSPDB:GN00023; CESP:W06A7.3b

A;Experimental source: clone W06A7

C;Genetics:



A;Gene: CESP:W06A7.3b  
A;Map position: 5  
A;Introns: 27/1; 77/2; 201/2

Query Match 5.7%; Score 340.5; DB 2; Length 222;  
Best Local Similarity 32.4%; Pred. No. 1.4e-07;  
Matches 66; Conservative 52; Mismatches 83; Indels 3; Gaps 2;

```
Qy      972 EKEDRSPSAIFSadL-GKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIA 1030
      :| : |: : : | || :|:|:| | | | :| :| :| :| :| :| :| :|
Db      9 KKYSKQPTWVPATDFPGK--ILDVIYWRDAKKSaIVLSLALLLVLFVLAKYPLLTVVVTYSL 66

Qy     1031 LALLSVTISFRIYKGVlQAIQKSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNCTIK 1090
      | | :|:| | | :|:| | | | :| :| :| :| :| :| :| :|
Db     67 LLALGAAAGFRVFKKVEAQIKKTdSEHPFSEILAQDLTLpQEKVHAQADVfVEHATCIAN 126

Qy     1091 ELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDH 1150
      :|:| | | :|:| | | :|:| | | | | :| :| | | :| :| | |
Db     127 KLKKLVFVESPLESIKfGLVLWSLTyIASWfSGFTLAILGLLGvFSVPKvYESNqEAIDP 186

Qy     1151 YLGLANKNVKDAMAKIQAKIPGLK 1174
      :| :|:| :| :| :| :|
Db     187 HLaTISGHLKNVQNIIDEKLpFLR 210
```

#### RESULT 7

I38346

elastic titin - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 21-Jul-2000

C;Accession: I38346

R;Labeit, S.; Kolmerer, B.

Science 270, 293-296, 1995

A;Title: Titins: giant proteins in charge of muscle ultrastructure and elasticity.

A;Reference number: A57430; MUID:96026330; PMID:7569978

A;Accession: I38346

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-7962 <RES>

A;Cross-references: EMBL:X90569; NID:g1017426; PIDN:CAA62189.1; PID:g1017427

C;Genetics:

A;Gene: GDB:TTN

A;Cross-references: GDB:127867; OMIM:188840

A;Map position: 2q31-2q31

Query Match 5.6%; Score 331; DB 2; Length 7962;  
Best Local Similarity 20.0%; Pred. No. 4.7e-05;  
Matches 235; Conservative 144; Mismatches 404; Indels 392; Gaps 48;

```
Qy      32 EDEEEEEEEEEDEDEDLEELE--VLERK---PAAGLSAAPV-----PTAPA 73
      |:| | | | | | | | :| | | :| :| :| :| :| :| :| :|
Db     6176 EEEREEEEEAeVTEyEVmEEPEEYvVEEKLHIISKrVEAEpAEVTERQeKKIVLkPKIPA 6235

Qy      74 AGAPLMDFGNDFVPPAPRGPLPAAP-PVAPERQPSWDPSVSSSTVPAPSPLSAAAVSPSK 132
      : | :| | | :|:| :| :| :| :| :| :| :| :| :|
Db     6236 K-----IEEPpPAKVPEAPKKIVPEKK-----VPAPVP-KKEKVppPK 6272
```

Qy	133	LPEDDEPPA---RPP-----PPPASVS-----PQAEPVWTPPAPAPAAPS-TPAA	175
Db	6273	VPEEPKKPVPEKKVPVKVIKMEELPAKVTEKHMQITQEEKVLVAVTKKEAPPKARVPEE	6332
Qy	176	PKRRGSSGAVVXXXXKIMDLK----EQPGNTISAGQEDF---PSVLLETAASXPS-LSPL	227
Db	6333	PKR-----AVPEEKVLKLPKREEEPPAKVTEFRKRVVKEEKVSIAPKREPQPIKEV	6385
Qy	228	SAASFKEHEYLGNLSTVLPTTEGLQEN-VSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	286
Db	6386	TIMEEKERAY-----TLEEEAVSVQREEEYEEYE---EYDYKEFEEYEPTTEE	6429
Qy	287	GSSFS-----VSPKAESAVIV--ANPREEI	309
Db	6430	YDQYEEYEEREYERYEEHEEYITEPEKPIPVKPVPEEPVPTKPKAPPKVLKKAVPEEKV	6489
Qy	310	IV----KNKDEEEKLVSNNILHXQQELPTALTCLKVKEDEVVSSEKAKDSFNEKRVAVEAP	365
Db	6490	PVPIPKKLKPPPPKVPEEPKKVFEEKIHISITK--REKEQVTEPAAKVPMKPKRVVAEEK	6547
Qy	366	MREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSE	425
Db	6548	VPVPRKEVAPPVRVPEVPKELEPEEV-----AFEEEVVTHVE-EYLVEEEEEEYIHEEE-E	6600
Qy	426	SSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFLLEDPTSENXTDEKKIEE	485
Db	6601	FITEEEVVPVIPVKVPE-----VPRKPVPEEKKPVVPVKKKEAPPKAVPEVPKKPEE	6652
Qy	486	KKAQIVTEKNTSTKTSNPF-----VAAQDSETDYVTTDNL-----	521
Db	6653	KVPVLIPKKEKPPPAKVPEVPKKPVPEEKVPVPVKKVEAPPKAVPEVPKKPVPEKKVPV	6712
Qy	522	-----TKVTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEV	571
Db	6713	PAPKKVEAPPKAVPEVPKKLIPEEKKPTVPVKKVEAPPKVPKKREPVPVPVALPQEEEV	6772
Qy	572	M-QESLYPAAQLCPSEFESEATP-----	593
Db	6773	LFEEEEIVPEEEVLP--EEEEVLPEEEVLPEEEVLPEEEIIPPEEEVPPPEEYVPEEE	6830
Qy	594	-----SPVLDPDIVMEAPLNSAVPSAGASVIQ-----PSSSPLEASSVNYESI-	635
Db	6831	EFVPEEEVLPEVKPKVPVPAPVPEIKKKVTEKKVVIKKEEAPPKAVPEVPKKVEEKRII	6890
Qy	636	--KHE-----PENPPPYEEAMSVSLKVSGIKEEI---KEPENIN	669
Db	6891	LPKEEEVLPEVTEEPPEEPISEEEIPEEPSIIEV-----EEVAPPRVPEVIK	6939
Qy	670	AALQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELVEDSSPDSEP	729
Db	6940	KAVPEAPTVP-----PKKVEAPP-----AKVSKKIPEEKVPVPVQKKEAPP	6980
Qy	730	VDLFSDDSIIPDPVQKQDETVMVLKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFK	789
Db	6981	A-----KVPEVPKKVPEKKVLV-----PKKEAVPPAKGR-----	7009

Qy 790 LSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFISKEAQIRETETFSDDSP 849  
 | : | : : | | : : | : : | : :  
 Db 7010 -----TVLEEKVSVAFRQEVVVKERLELEVVEAEVVE--IPEEEEFHEVEEYFEEGE 7059

Qy 850 IEIIDEFPTLISSKTDSFSKLAREYTDLEV--SHKSEIANAPDGAGSLPCTELPHDLSLK 907  
 : : | | : : : : : : | : : | : : : : |  
 Db 7060 FHEVEEFIKLEQHRVEEHRVEKVRVIEVFEEAEVEVFEEKPKAPPKGP-----EISEK 7113

Qy 908 NIQPK-----VEEKISFSDDFSKNKSATSKVLLLPDPVSAL 943  
 | | | | : : : : : : : :  
 Db 7114 IIPPKKPPTKVVPKPEPPAKVPEVPPKIVVEEKVRVPEE-----PRVPP----- 7157

Qy 944 GHTQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSP 978  
 : : : : | | | : | : : :  
 Db 7158 ----TKVPEVLPPK--EVVPEKKVPVPPAKKPEAP 7186

# RESULT 8

T13564

microtubule-associated protein homolog - fruit fly (*Drosophila melanogaster*)

N;Alternate names: hypothetical protein EG:49E4.1

C;Species: *Drosophila melanogaster*

C;Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 17-Nov-2000

C;Accession: T13564

R;Spanos, L.; Papagiannakis, G.; Siden-Kiamos, I.; Louis, C.

submitted to the EMBL Data Library, April 1999

A;Description: Sequencing the distal X chromosome of *Drosophila melanogaster*.

A;Reference number: Z17689

A;Accession: T13564

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-5327 <SPA>

A;Cross-references: EMBL:AL031128; PIDN:CAA20006.1

C;Genetics:

A;Cross-references: FlyBase:FBgn0025392

A;Introns: 24/2; 52/3; 104/3; 179/1; 232/1; 1669/3; 2566/1; 4798/3; 5272/1

A;Note: EG:49E4.1

C;Superfamily: *Drosophila* 576K microtubule-associated protein homolog

Query Match 5.5%; Score 325.5; DB 2; Length 5327;  
 Best Local Similarity 23.6%; Pred. No. 4.6e-05;  
 Matches 275; Conservative 151; Mismatches 520; Indels 219; Gaps 53;

Qy 28 VREPEDEEEEEEEEEEE---DEDEDLEELEVLERKPAAGLS-----AAPVPTAPAAG 75  
 : : : : | : : | : : | : : | : : | : :  
 Db 1277 MEQVKDKKEEHEQKIESGIITEKEAKKSASTPEEKETSDITSDDDELPAQLADPTTVPPKSA 1336

Qy 76 APLMDFGNDVFPPA-----PRGPLPAAPPV-APERQPSWDPSVPSSTVPAPSPLSAA 126  
 | | : | | : | | | | : | : : | | |  
 Db 1337 KDREDTGSIESPPTIEEAIEVEVQAKQEAQKVPAPAEAAIKTEKSPLASK-ETSRPESAT 1395

Qy 127 AVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPSTPA-----APK 177  
 : | | | | : : : : | : | : | : |  
 Db 1396 ----GSVKEDTEQTKSKKSPVPSRPESEAKDKKSPFASGEASRPESVAESVKDEAGKAES 1451

Qy 178 RRGSSGAVVXXXXKIMDLKEQPGNTISAGQE-----DFPSVLLETAASXP-SLSPLSA 229  
 | | | : | | | : | | | | : : |

Db 1452 RRESIAKTHKDESSLDKAKEQESRRESLAESIKPESGIDEKSALASKEASRPESVTDKS- 1510

Qy 230 ASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSS 289  
 || :: | | | : || | : : | | | :

Db 1511 ---KEPSRRESIAESLKAESTKDEKSAPPSKEASRPGSVVESVKDETEKSKEPSRRESIA 1567

Qy 290 FSVSPKAESAVIVANPREEIIVKNKDEEEKLVSN---ILHXQQELPTALTCLVKEDEVV 346  
 | | | : | | : | | | : : | : : | : :

Db 1568 ESAKPPIEFRE-VSRP-ESVIDGIKDESAKPESRRDSPLASKEASRPESVLESVKDEPIK 1625

Qy 347 SSEKAK-----DSFNEKRVAVE-APMREEYADFKPFERVWEVKDS--KEDSDMLAAGGKI 398  
 | : | : : : | | | : | : : : | | | : | | :

Db 1626 STEKSRRRESVAESFKADSTKDEKSPLTSKDIS-RPESAVENVMDAPFKETSRPESAVGSM 1684

Qy 399 ESNLESKVDKKCFADSLEQTNHE--KDSESSNDDTSFP-STPEGIKDRSGAYITCAPFNP 455  
 : || | : | | : : : | | | | | | | | | |

Db 1685 KDESMSK-----EPSRRESVKDGAQSRERSRPASVAESAkd--GADDLKELSRP 1732

Qy 456 AATE-----SIATNIFPLLEDPTS-----ENXTD--EKKIEEKKAQIVTEKN--TSTK 499  
 : | | | | : | | : | | | | : : | | : | :

Db 1733 ESTTQSKEAGSIKDEKSPLASEEASRPASVAESVKDEAEKSKEESRRESVAEKSPLPSKE 1792

Qy 500 TSNPFFVAAQDSETDYVTTDNLTQVTEEVVANMP---EGLTPDLVQEACESELNEVTGT 555  
 | | | | : | | | | | | | | | | : : |

Db 1793 ASRPASVA--ESIKDEAEKSKEESRRESVAEKSPLPSKEASRPASVAESIKDE-----AE 1845

Qy 556 KIAYETKMDLVQTSSEVM--QESLYPAAQLCPSFEESEATPSPVLPDIVME-APLNSAVPS 612  
 | | : : | : : : | : : : : : : : | | : | | |

Db 1846 KSKEESRRESVAEKSPLPSKEASRPASVAESIKDEAEKSKEESRRESVAEKSPLPSKEAS 1905

Qy 613 AGASVIQPSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSGIKEEI---KEPENIN 669  
 || | : | | : : | | : | : : | | : | |

Db 1906 RPASVAESIKDEAEKSKEESRRESVAEKSPLPSKEASRPASVAESIKDEAEKSKEESRRE 1965

Qy 670 AALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELVEDSSPDSEP 729  
 : : : | | | | | : : | | | | : | |

Db 1966 SVAEKSPLP-----SKEASRPASVAESIKDEAEKSKEE---SRRESVAEKSP---- 2009

Qy 730 VDLFSDDSIPDVPQKQDETVMVLVKESLTETSFESEMI--YENKEKLSALP-PEGGKP--Y 784  
 : | | : | | : : : | | : : | | | | : |

Db 2010 -----LPSKEASRPASVAESIKDEAEKSKEESRRESVAEKSPLPSKEASRPASV 2058

Qy 785 LESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQME--LSTAVYSNDDLFISKEAQIRE 840  
 | | | : : | : | | | | | : | | : | | |

Db 2059 AESIKDEAEKSK-----EESRRESAAEKSPLPSKEASRPASVAESVKDEADKSKEESRR- 2112

Qy 841 TETFSDDSSPIEII--DEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCT 898  
 | : : : | : | : : | : | | | | : | | :

Db 2113 -ESMAESGKAQSIKGDQSPLKEVSRPES---VAESVKDDPVKSK-EPSRRESVAGSVTAD 2167

Qy 899 ELPHDLSLKNIQPKVEEK-----ISFSDDFSNGSATSKVLLLLPPDVVSALGHTQAE 949  
 | : : | : | | | : | | : : |

Db 2168 -----SARDDQSPLESKGASRPESVVDVSKDEAEKQES-----RRESK 2205

Qy 950 IESIVKPKVLEKEAEKKL-----PSDTEKEDR-SPSAIFSADLGKTSVVDLLYW---RDI 1000  
 | : : | | : : : | : : : | | : : : | |

Db 2206 TESVIPPKAKDDKSPKEVLQPVSMETETIREDADQPMKPSQAESRRESIAESIKASSPRDE 2265

```

Qy      1001 KKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVQAIQKSDEGHPFR 1060
          |          | |          ||          : : | : : | | | | |
Db      2266 KSP-----LASKEASRPGSV-----AESIKYDLDPQIIKDDKSTE-HSRR 2305

Qy      1061 AYLESEVAI-SEELVQKYSNSALGH 1084
          || : | : || : | : : | |
Db      2306 ESLEDKSAVTSEKSVSRPLSVASDH 2330

```

# RESULT 9

A47282

calcium-binding protein calphotin - fruit fly (*Drosophila melanogaster*)

C;Species: *Drosophila melanogaster*

C;Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 21-Jul-2000

C;Accession: A47282

R;Martin, J.H.; Benzer, S.; Rudnicka, M.; Miller, C.A.

Proc. Natl. Acad. Sci. U.S.A. 90, 1531-1535, 1993

A;Title: Calphotin: a *Drosophila* photoreceptor cell calcium-binding protein.

A;Reference number: A47282; MUID:93165729; PMID:8094559

A;Accession: A47282

A;Status: preliminary

A;Molecule type: nucleic acid

A;Residues: 1-865 <MAR>

A;Cross-references: GB:L02111; NID:g157031; PIDN:AAA28405.1; PID:g157032

A;Experimental source: photoreceptor cells

A;Note: sequence extracted from NCBI backbone (NCBIN:124955, NCBIIP:124956)

C;Genetics:

A;Gene: FlyBase:Cpn

A;Cross-references: FlyBase:FBgn0010218

C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; von Willebrand factor type C repeat homology

C;Keywords: calcium binding

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Query Match          5.5%; Score 324.5; DB 2; Length 865;
Best Local Similarity 22.3%; Pred. No. 4.1e-06;
Matches 229; Conservative 128; Mismatches 375; Indels 297; Gaps 49;

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Qy      59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVVSSTVP 118
          | : | | | | | | | | : | | | | : | | | | : |
Db      9 PVSAPVAAPV-TPSAVAAPVQVVSPAAPVAPAPAAPIAVTPVAPPPTLASVQPATV--TIP 65

Qy     119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAP----APAAPP--ST 172
          ||:|:|:|:|:| | | | | | | : | | | | | : |
Db     66 APAPIAAASVTP---VASVAPPVVAAPTTPAA-SPVSTPVAVAQIPVAVSAPVAPPVAAT 121

Qy     173 PAAPKRRGSSGAVVXXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAASF 232
          | : : | : | | | | : | | | | : |
Db     122 PTPVVQIPVAAPVIAT-----PPVAASA-----PT----PAAVTPVISPVIAS-- 160

Qy     233 KEHEYLGNLSTVLPTTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSV 292
          |:| | | | : : | : : | : |
Db     161 -----PPVVPANTT----VPVAAPVAAPVAAVPVAPVLAP-----AV 194

Qy     293 SPKAESAVIVAN-----PREEIIIVKNKDEEEKLVSNILHXQQELPTALTCLKVKEDEVVS 347
          :| | :|| | || | :| : | : | ||:
Db     195 APAV--APVVAETPAPPPVAEIPVAT-----IPECVAPLIPEVSVVA 234

```

Qy 348 SEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVD 407  
 : | : | | | | | : : : | : : : |  
 Db 235 T---KPLAAAEPPVVAPPATET-----PVVAPAAASPHVSVAPAVETAVVAPVS 280

Qy 408 KKCFAADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFP 467  
 || : : | : | || ||  
 Db 281 -----ASTEPPV---AAATLTTPAPETPAL----- 301

Qy 468 LLEDPTSENXTDEKKIEEKKQAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTEE 527  
 | : | | || | | | |  
 Db 302 -----APVVAESQ-----VAA-----NTVVATPP 320

Qy 528 VVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPA----- 579  
 | || : | : | : | || : | || : | | || : ||  
 Db 321 TPAPEPETIAPPVV-----AETPEVASVAVA-ETTPPVV--PPVAAESI-PAPVVATTPV 371

Qy 580 -AQLCPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHE 638  
 | | : : | : | || : : || : | | : | : |  
 Db 372 PATLAVTDPDVTASAVPELPPVIAAPSPVPSAVAETPVDLAPPVLPPVAAEPVPAVVAEET 431

Qy 639 PENPPPYEEAMSV-SLKVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEP 697  
 || | | : : : | : : | | : | | : | : | : |  
 Db 432 PETPAPASAPVTIAALDIPEVAPVIAAPSDAPAEAPSAAPIVSTPPTTASVPETTAPPA 491

Qy 698 P-----DFSDYSEMAKVEQPVPDHSEL-----VEDSSPDSEPVDLFSDDSIIP--DVPQK 744  
 | | || | : | || | : | | : | | : | : |  
 Db 492 AVPTEPIDVSVLSE-AAIETPVAPPVEVTTEVAVADVAPPEAAADLIIPEVEPPAPIPDL 550

Qy 745 QDETVMLVKESLTETSFESMIEYENKEKLSALPPEGGKPYLESEFKLSLDNTKDTLLPDEV 804  
 : : | : | : : | : : || : : : : | : : |  
 Db 551 LEQTTSVPAVEAAESTSSPIPE-----TSLPPPNEAVASPEVAVAPITAPEPIPEPEP 603

Qy 805 STLSKKKEKIPLQ---MEELSTAVYSNDDLFISKEAQIRETETFSDDSPIEIIIDEFPTLI 860  
 | : | || : : : | || | : || | | | | || :  
 Db 604 SLATPTEPIPVVEAPVVIQEAVDVAV-----EVPVTETST---SIP-ETTVEFPEAV 649

Qy 861 SSKTDSFSKLAREYTDLEV-SHKSEIANAPDGAGSLPCTELP-----HDLSL 906  
 : | | : | : : : || || | || : | : :  
 Db 650 AEKV-----LDPATEAPVTTQEPDVANINDGA---PATEITTPAVEIVTAAAEVSDIAI 701

Qy 907 KNIQPKVEEKISFSDDFSNGSATSQVLL----LP-----PDVSALG----- 944  
 | | | : : : : : : : : : : | : ||  
 Db 702 PVIDPPVPQEIAVA-EIPETDTKPAEVIVEQSTIPIEAPVPEVSKYAEPVISEAPAAEVP 760

Qy 945 -----HTQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSADLGKTSVVDLLY 996  
 : | | : | | : || | : | : : || | | : | : ||  
 Db 761 ITAGDNPDNSTSVGISEVV-PTIAEKPVEEVPTSEIPEQSSSPSD--SVPVAK--ITPLL- 814

Qy 997 WRDIKKTGV 1005  
 || : | |  
 Db 815 -RDLQTTDV 822

RESULT 10  
 A47283  
 calphotin - fruit fly (Drosophila melanogaster)

C;Species: *Drosophila melanogaster*  
 C;Date: 21-Sep-1993 #sequence\_revision 25-Apr-1997 #text\_change 21-Jul-2000  
 C;Accession: A47283  
 R;Ballinger, D.G.; Xue, N.; Harshman, K.D.  
 Proc. Natl. Acad. Sci. U.S.A. 90, 1536-1540, 1993  
 A;Title: A *Drosophila* photoreceptor cell-specific protein, calphotin, binds calcium and contains a leucine zipper.  
 A;Reference number: A47283; MUID:93165730; PMID:8434015  
 A;Contents: photoreceptor cells  
 A;Accession: A47283  
 A;Status: preliminary  
 A;Molecule type: nucleic acid  
 A;Residues: 1-873 <BAL>  
 A;Cross-references: GB:L05080; NID:g157071; PIDN:AAA28420.1; PID:g157072  
 A;Note: sequence extracted from NCBI backbone (NCBIN:124958, NCBIP:124959)  
 C;Superfamily: collagen alpha 1(I) chain; fibrillar collagen carboxyl-terminal homology; von Willebrand factor type C repeat homology

Query Match 5.4%; Score 320.5; DB 2; Length 873;  
 Best Local Similarity 22.5%; Pred. No. 6e-06;  
 Matches 235; Conservative 122; Mismatches 367; Indels 321; Gaps 50;

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Qy      59 PAAGLSAAPV-PTAPAAGAPLMDFGNDVFPPAPRGPLPAAP----PVAPERQPSW-DPSP 112
      | : |||| |:| || :: | || | |||| ||| |: |
Db      9 PVSAPVAAPVTPSAVAAPVQVVSAAVAVAPAVVAPAPAAPTAVTPVAP--PPTLASVQP 66

Qy     113 VSSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPP-----A 163
      : |||||:|:|:|:|:| | | | | | | | | |
Db     67 ATVTVPAPIAAASVAP---VASVAPPVVAAPTTPA-----ASPVSTPPVAVAQIPVAV 118

Qy     164 PAPAAPP----STPAAPKRRGSSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLET-- 217
      || ||| | | || ::| | |
Db     119 SAPVAPPVAATPTPVAP-----IPVAAPVIATPPVAASAPT 154

Qy     218 -AASXPSLSPLSAAAFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLT 276
      || | :|:| | :| | | : : | : |
Db     155 PAAVTPVVSPVIAT-----PPVVPANTT---VPVAAPVAAVPAVPVAVPLA 199

Qy     277 EFSELEYSEMGSSFSVSPKAESAVIVAN-----PREEIIVKNKDEEEKLVSNILHXQQE 331
      :|:| | :| | | || |
Db     200 P-----AVAPAV--APVVAETPAPPPVAEIPVAT----- 226

Qy     332 LPTALTKLVKEDEVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDM 391
      :| : |:| ||:| | : | | | | | | |
Db     227 IPECVAPLIPEVSVVAT---KPLAAAEVVPVAPPATET-----PVVAPAAASPH 272

Qy     392 LAAGGKIESNLESKVDKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCA 451
      :: :|: : : | || : : | :| |
Db     273 VSVAPAVETAVVAPVS-----ASTEPPV---AAATLTTA 303

Qy     452 PFNPAATESIATNIFPLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDS 511
      | || | :| | |||
Db     304 PETPAL-----APVVAESQ-----VAA--- 320

Qy     512 ETDYVTTDNLTQVTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEV 571
      | | | ||:|:| :| || :| || :|
Db     321 -----NTVVATPPTPAPEPETIAPPVV-----AETPEVASVAVA-ETTPPVV--PPV 364

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Qy 572 MQESLYPA-----AQLCPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPS 622  
 ||: || | | : : | : | || : : || | : |  
 Db 365 AAESI-PAPVVATTPVPATLAVTDPDVTASAVPELPPVIAPSVPSAVAETPVDLAPPVL 423

Qy 623 SPLEASSVNYESIKHEPENPPPYEEAMSV-SLKVSGIKEEIKEPENINAALQETEAPYIS 681  
 |: | | : || | : : : | : | : | || : |  
 Db 424 PPVAAEPVPAVVAEETPETPAPASAPVTIAALDIPEVAPVIAAPSDAPAEAPSAAPIVS 483

Qy 682 IACDLIKETKLSAEPAP-----DFSDYSEMAKVEQPVPDHSEL-----VEDSSPDSEPV 730  
 : : || | | || | : || | : | | : |  
 Db 484 TPPTTASVPETTAPPAAVPTEPIDVSVLSE-AAIETPVAPPVEVTTEVAVADVAPPEAAE 542

Qy 731 DLFSDDSSIP--DVPQKQDETVMVLKESLTETSFESMIEYENKEKLSALPPEGGKPYLESF 788  
 || : | : | : : | : : | : : ||  
 Db 543 DLIIEPVEPPAPIPDLLLEQTTSVPAVEAAESTSSPIPE-----TSLPPPNEAVASPEV 595

Qy 789 KLSLDNTKDTLLPDEVSTLSKKEKIPLQ---MEELSTAVYSNDDLFIKSEAQIRETETF 844  
 : : : : | | : | || : : | | | : | | |  
 Db 596 AVAPITAPEPIPEPEPSLATPTEPIPVVEAPVVIQEAVDV-----EVPVTETST- 644

Qy 845 SDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEV-SHKSEIANAPDGAGSLPCTELP-- 901  
 | | | ||| : : | | : | : : || || | || :  
 Db 645 --SIP-ETTVEFPPEAVAQKV-----LDPATEAPVTTQEPDVANINDGA---PATEITTP 693

Qy 902 -----HDLSLKNIQPKVEEKISFSDDFSNGSATSKVLL-----LP-----PDVS 941  
 | : : | | | : : : : : : : : : : : | : ||  
 Db 694 AVEIVTAAAEVSDTAIPLIDPPVPQEIAVA-EIPETETKPAEVIVEQSTIPIEAPVPEVS 752

Qy 942 ALG-----HTQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSA 980  
 : | | : | | : | | : | : : ||  
 Db 753 KYAEPVISEAPAAEVPITAGDNPNTSVGISEVV-PTIAEKPVEEVPTSEIPEQSSSPSD 811

Qy 981 IFSADLGKTSVVDLLYWRDIKKTGV 1005  
 | : | : || || : | |  
 Db 812 --SVPVAK--ITPLL--RDLQTTDV 830

RESULT 11

T34418

hypothetical protein F12F3.3 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 29-Oct-1999

C;Accession: T34418

R;Fulton, B.; Wohldmann, P.

submitted to the EMBL Data Library, July 1998

A;Description: The sequence of *C. elegans* cosmid F12F3.

A;Reference number: Z21521

A;Accession: T34418

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-3488 <FUL>

A;Cross-references: EMBL:U80022; PIDN:AAC25885.1; GSPDB:GN00023; CESP:F12F3.3

A;Experimental source: strain Bristol N2; clone F12F3

C;Genetics:

A;Gene: CESP:F12F3.3

A;Map position: 5



A;Introns: 281/3; 332/1; 562/3; 600/3; 1866/3; 1944/3; 3393/1

Query Match 5.1%; Score 299.5; DB 2; Length 3488;  
Best Local Similarity 20.6%; Pred. No. 0.0003;  
Matches 272; Conservative 187; Mismatches 475; Indels 387; Gaps 57;

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Qy      1 MEDLDQSPLV--SSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEV---- 54
      ::::| | ::      | : :| | : ::| | | :      | | : : |::|
Db      340 VDEVDDSTVLEEKDDGDDKSKPKTKKKI I KKKETPESEQVTAAEPEQQKISEVDVQSV 399

Qy      55 -----LERKPAA---GLSAAPVPT-----APAAGA-----PLMD-----FGNDF 85
      :|| |      || | :      | |      | |
Db      400 ETEVGAKKKPDAEKPTDLSKAKKDSKSKSDEPEASTEESTTEKPTNDKTSKKSAAEKT 459

Qy      86 VPPAPR---GPLPAAPPVAPERQPSWDPSVVSSTVPA-----PSPLSAAAV 128
      | |      || | || : : | | | : |      | :| :
Db      460 VKPKKEVTGKPLEAKKPVEDKKDASQPSSSKESPPTDGKKKKQIPKALFIPDEISSRFG 519

Qy      129 SPSKL-----PEDDEPPARPP--PPPPASVS-----PQAEPVWTPPAP 164
      || :      :      | : | | |||      :| | : :
Db      520 DPSTMHSETNITTTIRGREGSADAKTPLVEPLSASVSMKVFTLVESAKEAEFSFKRRSE 579

Qy      165 AP-----AAPPSTPAAPK-----RRGSSGAVVXXXXKIMD-----LKEQPGN----- 201
      |      || : : |      : | :| :| | :| :| :| :
Db      580 TPDDKSRKKEGLPPAKKSEKKDEVTAEQSTEALIESKKKEVDESKISEQQPSDKNKSEV 639

Qy      202 ----TISAGQEDFPSVLLETAASXPSLSPLSAAAFKEHEYLGNLSTVL---PTEGTLQEN 254
      :|| |      |      : : | :      | || : : :
Db      640 VGVPEKAAGPETKKDV--SEIEEVPKKKTIKKKTEKSDSSISQKSNVLKPADDDKSKSD 697

Qy      255 VSEASKEVSEKAKTLLID-----RDLTEFSELE-----YSEMGSSFVSVP 294
      |:: ||: :| : : |      | | : | |      :| || :|
Db      698 VTDKSKKTTEDQTKVATDSKLEKAADTTKQIETETVDDKSKKKVLKKKTEKSDSF-ISQ 756

Qy      295 KAESAVIV--ANPRE----EIIIVKNKDEEEKLVSNILHXQQELPTALTCLKVED----- 343
      |:| : :| | : :| || ::| | :| : :| | | : |
Db      757 KSETPPVVEPTKPAESEAQKIAEVNKAQKQEVDDNL---KREA EVAAKKIADKLEKIEA 813

Qy      344 -----EVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAG 395
      || ::| | : : : : | : : | : :| : | |
Db      814 EANIKKTAEEVAACKQKEKDEQLKLETEVVSKKSAAEKLELEKQAIKKAEEAD---AVK 870

Qy      396 GKIESNLESKVD--KKCFAD--SLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCA 451
      : | | ::| : : || || || : : | : | : | | | :|
Db      871 KQKELNEKNKLEAAKSAADKLKLEESAASKKVVSEESVKF---GEEKTKAGEKTVQV 927

Qy      452 PFNPAATESIATNIFPLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDS 511
      | : ::| | | | | | :||| :|| ||| :| : :| |
Db      928 ESEPTSKKTIDTKDVGATE-PADE--TPKKKI I KKK---TEKSDSS-----ISQKS 972

Qy      512 ETDYVTTDNLTKVTEEVVANMPEGLTPDLVQEACESELNEVTGTK-----IAYETKMDL 565
      || : : :| | :      | : || :| : : | | || :| :
Db      973 ATD---SEKVSQKEQDEPTKPAVSETQMVTADKSKKQKETDEKLKLD AEIAAKTKQEA 1029

Qy      566 VQTSEV-MQESLYPAAQLCPSFEESEATPSPVLPD-IVMEAPLNSAVPSAGASVIQPSSS 623
      : |:: || : :      | : | | : :| : : | | : : :
Db      1030 DEKSKLDAQEKIKKVS-----EDDAARKEKELNDKLESEIATKKASADKLKLEEQAQ 1083
```

Qy 624 PLEASSVNYESIKHEPENPPPYE-EAMSVSLKVSGIKEEIKEPENINAALQETEAPYISI 682  
 :|: | |: | : | : : : | | : | |:: | | :  
 Db 1084 AKKAAEV--EAAKKQKEKDEQLKLDTEAASKKAAAEKLELEKQAQIKKA---AGADAVKK 1138  
 Qy 683 ACDLIKETKLSAEPAPDFS----DYSEMAKVEQVPDPHSEL-----VE 721  
 :| :: || | : || :| | : ::| |  
 Db 1139 QKELDEKNKLEANKKSAAGKLKIEEESAASKQTVEEQAKLDAQTKAKTAEKQTKLEKDE 1198  
 Qy 722 DSSPDSEPVDLF-----SDDSI-----PDVP 742  
 |: :|| : || || |  
 Db 1199 KSTKESESKETVDEKPKKKVLKKKTEKSDSSISQKSETSKTVVESAGPSESETQKVADAA 1258  
 Qy 743 QKQDET-----VMLVKESLTETSFESMIEYENKEKLSA-----LPP 778  
 :|| || : |:| | :| :| |:| | :| |  
 Db 1259 RKQKETDEKQKLEAEITAKKSADE---KSKLEAESKLKAAEVEAAKKQKEKDEQLKLD 1315  
 Qy 779 EGGKPYLESFKLSLDNTKDTLLPDEVSTLSKK-----EKIPLQME 818  
 | : || |: || : |: ||: |: :  
 Db 1316 EAASKKAAAEKLELEKQSHIKKAAEVDVKKQKELEEKQRLSEEAATKKADAELKLEEQ 1375  
 Qy 819 ELSTAVYS-----NDDLFIKSEAQIRETETFS---DSSPIEIIDEFP 857  
 : | : :| :| | |:| | : :| | :|| |  
 Db 1376 KKKAEEIALIEIQKEQEKLAEQSRLEDEAKKSAEKQKLESETKSKQTEEAPKESVDEKP 1435  
 Qy 858 --TLISSKTDSFSKLAREYTDLEVSHKSEIANAP-DGAGSLPCTELPHDLSLKNIQPKVE 914  
 : : || | :| :| ||: | : | | :| | :| | ||  
 Db 1436 KKKVLKKKT-----EKSDSSISQKSKSAKSTVDAAETL---ESDFNLVEKKTQKVE 1484  
 Qy 915 -----EKISFSDDFSNGSATSKVLLLLPPDVSA LGHTQAEIESIVK 955  
 |::| || : : | | | | : :||  
 Db 1485 QSPDESTSATIKRDPAQKTEEISKQDDGDEKKT TTDGKPPKPEDSEA----TPKKRVVK 1539  
 Qy 956 PK-----VLEKEAEKKLPSDTEKEDRSPSAIF SADLGKTSVVD 993  
 | | || :| | ||| | | | | | :  
 Db 1540 KKTQKSDSVASDASLADVSKLSDDVEEKPKKKVLKKKTEKSDSVISETSSVDTIKPESVE 1599  
 Qy 994 L 994  
 :  
 Db 1600 I 1600

# RESULT 12

S37431

ankyrin 2, neuronal long splice form - human

N;Alternate names: ankyrin B, 440K splice form; ankyrin-B; brain ankyrin; non-erythroid ankyrin

N;Contains: ankyrin 2, short form

C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 13-Aug-1999

C;Accession: S37431; A39643; B39643; A40334; A49462; S14533; S14569

R;Chan, W.

submitted to the EMBL Data Library, September 1993

A;Reference number: S37431

A;Accession: S37431

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-3924 <CHA>  
 A;Cross-references: EMBL:Z26634; NID:g406287; PIDN:CAA81387.1; PID:g406288  
 R;Otto, E.; Kunitomo, M.; McLaughlin, T.; Bennett, V.  
 J. Cell Biol. 114, 241-253, 1991  
 A;Title: Isolation and characterization of cDNAs encoding human brain ankyrins  
 reveal a family of alternatively spliced genes.  
 A;Reference number: A39643; MUID:91302466; PMID:1830053  
 A;Accession: A39643  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-2077 <OT1>  
 A;Cross-references: GB:X56957  
 A;Accession: B39643  
 A;Status: preliminary  
 A;Molecule type: mRNA  
 A;Residues: 1-1443,3585-3924 <OTT>  
 A;Cross-references: EMBL:X56958  
 R;Tse, W.T.; Menninger, J.C.; Yang-Feng, T.L.; Francke, U.; Sahr, K.E.; Lux,  
 S.E.; Ward, D.C.; Forget, B.G.  
 Genomics 10, 858-866, 1991  
 A;Title: Isolation and chromosomal localization of a novel nonerythroid ankyrin  
 gene.  
 A;Reference number: A40334; MUID:92009921; PMID:1833308  
 A;Accession: A40334  
 A;Molecule type: DNA  
 A;Residues: 463-474,'PE',477-495 <TSE>  
 A;Cross-references: GB:M37123; NID:g178647; PIDN:AAA62828.1; PID:g178648  
 R;Chan, W.; Kordeli, E.; Bennett, V.  
 J. Cell Biol. 123, 1463-1473, 1993  
 A;Title: 440-kD ankyrinB: structure of the major developmentally regulated  
 domain and selective localization in unmyelinated axons.  
 A;Reference number: A49462; MUID:94075409; PMID:8253844  
 A;Accession: A49462  
 A;Status: preliminary; nucleic acid sequence not shown  
 A;Molecule type: mRNA  
 A;Residues: 1-3924 <RES>  
 A;Cross-references: EMBL:Z26634; NID:g406287; PIDN:CAA81387.1; PID:g406288  
 C;Genetics:  
 A;Gene: GDB:ANK2  
 A;Cross-references: GDB:127607; OMIM:106410  
 A;Map position: 4q25-4q27  
 C;Superfamily: ankyrin; ankyrin repeat homology  
 C;Keywords: alternative splicing  
 F;2-3924/Product: ankyrin 2, long form #status predicted <MAT>  
 F;2-1443,3585-3924/Product: ankyrin 2, short form #status predicted <MA2>  
 F;63-95/Domain: ankyrin repeat homology <AN01>  
 F;96-128/Domain: ankyrin repeat homology <AN02>  
 F;129-161/Domain: ankyrin repeat homology <AN03>  
 F;162-190/Domain: ankyrin repeat homology <AN04>  
 F;191-223/Domain: ankyrin repeat homology <AN05>  
 F;232-264/Domain: ankyrin repeat homology <AN06>  
 F;265-297/Domain: ankyrin repeat homology <AN07>  
 F;298-330/Domain: ankyrin repeat homology <AN08>  
 F;331-363/Domain: ankyrin repeat homology <AN09>  
 F;364-396/Domain: ankyrin repeat homology <AN10>  
 F;397-429/Domain: ankyrin repeat homology <AN11>  
 F;430-462/Domain: ankyrin repeat homology <AN12>

F;463-495/Domain: ankyrin repeat homology <AN13>  
 F;496-528/Domain: ankyrin repeat homology <AN14>  
 F;529-561/Domain: ankyrin repeat homology <AN15>  
 F;562-594/Domain: ankyrin repeat homology <AN16>  
 F;595-627/Domain: ankyrin repeat homology <AN17>  
 F;628-660/Domain: ankyrin repeat homology <AN18>  
 F;661-693/Domain: ankyrin repeat homology <AN19>  
 F;694-726/Domain: ankyrin repeat homology <AN20>  
 F;727-759/Domain: ankyrin repeat homology <AN21>  
 F;760-792/Domain: ankyrin repeat homology <AN22>  
 F;793-825/Domain: ankyrin repeat homology <AN23>

Query Match 5.0%; Score 299; DB 2; Length 3924;  
 Best Local Similarity 21.5%; Pred. No. 0.00037;  
 Matches 258; Conservative 167; Mismatches 417; Indels 358; Gaps 62;

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Qy      14 DSPP-----RPQPAFKYQFVREPEDEEEEEEEEEDEDEDLE-----ELEVLERK 58
      | ||           :| | | :| :| :| :| :| :| :| :| :| :| :| :| :|
Db      1648 DIPDETQSTQKQHKPSLGIKKPVRRKLKEKQKQKEEGLQASAEKAEKKGSSSEESLGED 1707

Qy      59 PAAGLSAAPVPTAPAAGAPLMD-----FGNDFVPPAPRG----- 92
      | ||: |:|| | :||:| :| :| :| :| :| :| :| :| :| :| :|
Db      1708 P--GLAPEPLPTVKAT-SPLIETPIGSIKDKVKALQKRVEDEQKGRSKLPPIRVKGKEDV 1764

Qy      93 -----PLPAA-PPVAPERQPSWDPS-----VSSTVPAPSPL 123
      | ||| | : || || || || || || || || || || || || || || ||
Db      1765 PKKTTHRPHPAASPSLKSERHAPGSPSPKTERHSTLSSSAKTERHPPVSPSSKTEKHSPV 1824

Qy     124 SAAA-----VSPSKLPEDDEPPA-----RPPPPPPASVSPQAEPVW 159
      | :| || || | | : | || | : : : ||
Db     1825 SPSAKTERHSPASSSSKTEKHSPVSPSTKTERHSPVSSTKTERHPPVSPSGKTDKRPPV- 1883

Qy     160 TPPAPAPAAPSTPAAPKRR---GSSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLE 216
      :| || :| :| :| || || || :| :| :| :| :| :| :| :|
Db     1884 SPSGRTEKHPPVSPGRTEKRLPVSPSGRTD-----KHQPVSTAGKTEKHLVPVSPSG 1934

Qy     217 TAASXPSLSPLSAAS-FKEHEYLGNLSTVLPT-----EGTLQENVSEASKEVSEKAKT 268
      | :|| | :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db     1935 KTEKQPPVSPTS KTERIEETMSVRELMKAFQSGQDPSKHKTGLFEHKSQKQKQKQKGV 1994

Qy     269 -----LLIDRDLTEFSELEYSEMGSFSVSPKAES--AVIVANPREEIIVKNKDE-- 316
      :| | : : :| : :| | : || | | : : | || :|
Db     1995 RVEKEKGPILTQRE-AQKTENQTIKRGQRLPVTGTAESKRGVRVSS----IGVKKEDAAG 2049

Qy     317 -EEKLVSNNI-----LHXQQELPTALTCLVKE-----DEVV 346
      :||:| :| | :| :| :| :| :| :| :| :| :| :| :| :| :|
Db     2050 GKEKVLSHKIPEPVQSVPEEESHRESEVPK--EKMADEQGDMDLQISPDRTSTDFSEVI 2107

Qy     347 SSE-KAKDSFNEKRVAVEAPMREEYAD---FKPFERVWEVKDSKED----- 388
      | : | : :| :| : :| || : :| :| :| :| :| :| :| :|
Db     2108 KQELENDKYQQFRLSEETEKALHLQVLTSPFNNTTFPLDYMKDEFLPALSLQSGALDG 2167

Qy     389 -SDMLAAGGKIESNLESKVDKKCFADSLEQTNHE---KDSSESNDDTSFPSTPEGIKDRS 444
      | : | | | : : | | || : | :| :| :| :| :| :| :| :| :|
Db     2168 SSELKNEGVAGSPCGSLMEGTPQISSEESYKHEGLAETPETSPELSF--SPKKSEEQT 2225

Qy     445 GAYITCAPFNPAATESIATNIFLLEDPTSENXTDEKKIEEKKAIQIVTEKNTSTKTSNPF 504

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      |           :       | |       | |::: |       ||: | : : | |:::
Db      2226 G-----ETKESTKTETTTTEIRSEKEHPTTKDITGGS--EERGATVTEDESSTESFQKE 2277

Qy      505 FVAAQDSETDYVTTDNLTQVTEEVVA-NMPEGLTPDLVQEACESELNEVTGTKIAYETKM 563
      : |       | : |       : |       | | |       : | |       | : | : |
Db      2278 ATLGSPKDTSPKRQDDCTGSCSVALAKETPTGLT----EEAACDEGQRTFGSS-AHKT-- 2330

Qy      564 DLVQTSEVMQESLYPAAQLCPSFEESEATPSPVL-----PDIVMEAP--LNSAV 610
      ||       || |       : : | : | | |       | | : : | | | :
Db      2331 ---QTDSEAQES-----TATSDETKALPLPEASVKTDGTESKPQGVIRSPQGLELAL 2380

Qy      611 PSAGASVIQ-----PSSSPLEASSVNYESIKHE-PEN---PPPYEEA-MSVSLKVSG 657
      || : | :       | | | | | : : | : | : | | : | : | : |
Db      2381 PSRDSEVL SAVADDSLAVSHKDSLEASPVLEDNSSHKTPDSLEPSPLKESPCRDSSLESSP 2440

Qy      658 IKEEIKE---PEN--INAAEQETE--APYISIACDLIKETKLSAEPAPDFSDYSEMAKVE 710
      : : : | | : : | : | : | | | : | : | : | | : | : |
Db      2441 VEPKMKAGIFPSHFPLPAAVAKTELLTEVASVRSRLLRD-----PDGS--AEDDSLE 2490

Qy      711 QPVPDHSELVEDS-----SPDSEPVDLFSDDSI DPVPQKQDETVMVLKESLTETS FESMI 765
      |       : | : | | | : : | : | : | : | : | : |
Db      2491 Q-----TSLMESSGKSPSPDTPSSEEVSYEVTPKTTDVSTPKPAVIHECAEED----- 2539

Qy      766 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKK----EKIPLQMEELS 821
      : | | | | | | | | : | : | : | : | : | : | : |
Db      2540 DSENGEKKRFTPEE-----EMFKMV---TKIKMF-DELEQEAQKRDYKKEPKQEESSS 2589

Qy      822 TAVYSNDDLFIKSEA-QIRETETFTSDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVS 880
      : | : | | : : : | : | : | : | : | : | : | :
Db      2590 S---SDPDADCSVDVDEPKHTGSGEDES GV-----PVLVTSES RKVSSSES----- 2633

Qy      881 HKSEIANAPDGAGS-----LPCTELPHDL SLKN-----IQPKVEEKISF--SDD 922
      : | : | | | | | | : | : | : | : | : | : | : |
Db      2634 -EPELAQLKKGADSGLLPEPVIRVQPPSPPLSSMDSNSSPEEVQFQPVVSKQYTFKM NED 2692

Qy      923 FSKNGSATSKVLLLPDVSALGHTQAEIESIVKPKVLEKEAEKKLPD-----TEKEDRS 977
      : : : | : : | : | : | : | : | : | : | : |
Db      2693 TQEEP GKSEE-----EKDSESHLAEDRHAVSTEAEDRS 2725

```

RESULT 13

T16251

hypothetical protein F35A5.1 - *Caenorhabditis elegans*

C;Species: *Caenorhabditis elegans*

C;Date: 20-Sep-1999 #sequence\_revision 20-Sep-1999 #text\_change 18-Feb-2000

C;Accession: T16251

R;Leimbach, D.

submitted to the EMBL Data Library, January 1996

A;Description: The sequence of *C. elegans* cosmid F35A5.

A;Reference number: Z18485

A;Accession: T16251

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-1274 <LEI>

A;Cross-references: EMBL:U46675; NID:g1166613; PID:g1166621; PIDN:AAB52641.1;

GSPDB:GN00028; CESP:F35A5.1

A;Experimental source: strain Bristol N2; clone F35A5

C;Genetics:  
A;Gene: CESP:F35A5.1  
A;Map position: X  
A;Introns: 1272/2

Query Match 4.9%; Score 290.5; DB 2; Length 1274;  
Best Local Similarity 20.5%; Pred. No. 0.00017;  
Matches 221; Conservative 126; Mismatches 417; Indels 313; Gaps 45;

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Qy      13 SDSPPRP--QPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPAAGLSAAPVPT 70
      | :|| |  || |:: | |||| |  ||:  ||:|:  ||
Db      2 SRAPPTPIKNPAKKWKPPWESVDEEEEME-----VDEETPAPSKLEKKPSLKRKDAPTKP 56

Qy     271 APAAGAPLMDFGNDVFPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAPSPLSAAAVSP 130
      | : |||  | :|  || : | | | :  ||  |
Db     57 VPSPGAP-----SPVPIKNPVKKWKAPWEDDEPFMEEAAP-----VP 94

Qy    131 SKLPEDDEP---PARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRGSSGAVVX 187
      :|  |  |  ||:|  | :  :  |  || || ||  :
Db     95 AKKVRDPSPKKVPAKPRDASPKKIMAAKK----EPETLPAVPP-TPVKNPVKKFKAPWED 149

Qy    188 XXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXP-SLSPLSAASFKEHEYLGNLSTVLP 246
      : |:|: |  |: | :  ||: |  || || |||: :  | |
Db    150 DEVDVEDVKDAP--TVPAAKTPVLKKKEFAAAAKPRDPSPKKAAPSKEHDPI-----VPP 202

Qy    247 TEGTLQENVSEASKEVSEKAKTLLIDRDL--TEFSELE-----YSEMSSFSVSPKA 296
      |  |  |  | :|| |  | :|  | | |  :  | || | :
Db    203 T-----PIKNPAKKWKPPWEDDEVPTEEIKEPEPATRKVPALKKKEPSTSVKPKVS 252

Qy    297 ESAVIVANPREEIIVKNKDE-----EKLVSNNILHXQQELPTALTKL 339
      :  :  | :|: || : |  |::  :  :  :|  :
Db    253 D-----PSPTKKVPVKKEPEVPPTPIKNPTKKWKPPWEDETPEEVV--KEPPVPEKKAPV 305

Qy    340 VKEDEVVSSEKAKDSFNEKR-----VAVEAPMREEYADFKPFERVWEVKDSKEDS 389
      |:| :  : ||:|  |  |  |::  :||  ||| |  :
Db    306 LKKKDPAAPAKARDPSPSKAAPKKVEPSSPVVPPTPVKNPVKKYKP---PWEVDDEPAE- 361

Qy    390 DMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYIT 449
      |  |  | :||  |::  | | : : | |  :| | :
Db    362 -----EVKKPSAPEKK--TPVLKRKEPEPSSTTPSSDSPKKAAPAVKPRDSSPKK 410

Qy    450 CAPF--NPAATESIATNIFPLLEDPTSE-----NXTDEKKIEE-KKAQIVTEKNTSTKTS 501
      |  :| | |  | :  :|| :  || :|| |: :  :|  |
Db    411 ATPLQADPKAQEVPTPV----KNPVKKYKPPWEVDDEDPVEEVKQPEAPAKKTPVLKRK 466

Qy    502 NPFFVAAQDSETDYVTTDNLTKVTEEVVANMPE-----GLTPDLVQ---- 542
      |  ||:|  |  | | |  ||  | |
Db    467 EP---AAKD-----TAKPATSKTPET---PEKKDPVKPRDSSPKKVAAPKPSAQAPAT 513

Qy    543 -----EACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEES 589
      |  | : :|:  | :|  :  :|| | |  :
Db    514 PVKNPVKKWRPPWEDDETPADDVSKPTDAKKTPSLAKKDPAPAKESLKPKADTKAPAKPR 573

Qy    590 EATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYEEAM 649
      : :|  | |  |  | :  | |  | | :| :| | :
Db    574 DSPSKKVAP-----TAPEKKTPLAKKEPAGPADSKTKEPEKSKPRDPSPKKAVP 623
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QY      650 S-----VSLKVSGIK--EEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSD 702
      :      :      :      :      :      :      :      :      :      :      :
Db      624 AKVPVKTEVAPAAVKKPEPISKPKDTAPKKAEPNSPVV-----PPTP----- 665

QY      703 YSEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMILVKESLTETSFE 762
      |: ||      ||      :|| |      |: : : | :| ||: | : |
Db      666 -----VKNPVKKWKPPWEDDDAPAKPVSL-----PEPEKKTPLAKKAPTTPDSE 710

QY      763 SMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELST 822
      :| | |
Db      711 -----AAADPVSGP----- 719

QY      823 AVYSNDDLFISKEAQIRETETFSDDSSPIEII-----DEFPTLISSKTDSEFSLAREYT 875
      |: | :||:| ::      | ||:: :      | | : | : :|
Db      720 ---SSKDPKLAKKAPVKP----RDPSPMKAVPIKPAPKTEVPPAVVKKPEPVAK----- 766

QY      876 DLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVE-----EKISFSDDFSNGSA 929
      : | | | | : : | | | :| :| | | : : : |
Db      767 SRDPSPKK--AKAEPNSPVVPPT--PVKNPVKKWKPPWEDDDAPAEFPVNVPEPEKKTPL 822

QY      930 TSKVLLLPPDVS-----ALGHTQAEIESIVKPKVLEKEAEKKLPDTEKEDRSP 978
      | : | | | | | | | : ||: : | | | | : | ||
Db      823 AKKTPVKPRDPSPKKAVPAKPSTKTDAPPVSVKKPEPVSKPKE---PSPKKAEPNSP 876

```

# RESULT 14

A56577

microtubule-associated protein MAP 1B - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 21-Jul-1995 #sequence\_revision 21-Jul-1995 #text\_change 16-Feb-1997

C;Accession: A56577

R;Zauner, W.; Kratz, J.; Staunton, J.; Feick, P.; Wiche, G.

Eur. J. Cell Biol. 57, 66-74, 1992

A;Title: Identification of two distinct microtubule binding domains on recombinant rat MAP 1B.

A;Reference number: A56577; MUID:92347374; PMID:1639092

A;Accession: A56577

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-2364 <ZAU>

A;Cross-references: GB:X60550

A;Experimental source: brain

A;Note: nucleotide sequence not given; conceptual translation not complete

C;Superfamily: microtubule-associated protein MAP1B

Query Match 4.9%; Score 289; DB 2; Length 2364;

Best Local Similarity 20.9%; Pred. No. 0.00047;

Matches 275; Conservative 158; Mismatches 462; Indels 422; Gaps 61;

```

QY      30 EPEDEEEEEEEEEDEDEDLEELEVLERKPAAGLSAAPVPTAPAAGAPLMDFGNDFVPPA 89
      | | ||| ||||: : || : : | | | | : ||:
Db      909 EAEQSEEEGEEEEEDKAEDAREEDHEPDKTEAEDYMAVVDKAAEAGVTEDQY---DFL--- 963

QY      90 PRGPLPAAPP--VAPERQPSWDPSPVSSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPP 147
      || | :| ||: | | :| | | | | :| |
Db      964 ---GTPAKQPGVQSPSREPA--SSIHDETLPGGSESEATA-----SDEENREDQPEEF 1011

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QY	148	PASVSPQAEFPVWTPPAPAPAAPSTPAAPKRRGSSGAVVXXXXKIMDLKEQPGNTISAGQ	207
Db	1012	TATSGYTQSTIEISSSEPTPMDEMSTP-----RDVMTDETNNREETESPSQ	1055
QY	208	E-----DFPSVLLETAASXP---SLSPLSAASFKE---HEYLGNLSTVLPTEGTLQENV	255
Db	1056	EFVNITKYESSLYSQEYSKPVVASFNGLSDGSKTDATEGRDYNASASTISPPSSMEEDKF	1115
QY	256	SEAS-----KEVSEK-----AKTLLIDRDLTE	277
Db	1116	SKSALRDAYRPEETDVKTGAELDIKDVSDERLSPAKSPSLSPSPSPSIEKTPLGERSV-N	1174
QY	278	FS----ELEYSEMGSFS-VSPKAESAVI---VANPRE---EIIVKNK-----	314
Db	1175	FSLTPNEIKASAEGEATAVVS PGVTQAVVEEHCASPEEKTLEVVSQS SVTGSAGHTPY	1234
QY	315	----DEEEKLVSNILHXQQELPTALT KL VKEDEVSSE--KAKDSFNEKRVAVEAPMRE	368
Db	1235	QSPTDEKSSHLPTTEVTENAQAVP-----VSFEFTEAKDE-NER--SSISPMDE	1279
QY	369	EYADFK-PFERVWE-----VKDSKED---SDMLAAGGKIESNLESKVDDKKCFADSL	415
Db	1280	PVPDESPIEKVLSPLRSPPLIGSESAYEDFLSADDKALGRRESPEFGKNGKQGFSD--	1337
QY	416	EQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNP--AATESIATNIFPLLED-	471
Db	1338	-----KESPVS-DLTS DLYQDKQEEKRAGFIPIKEDFSPEKKASDAEIMSSQSALALDE	1390
QY	472	-----PTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTK	523
Db	1391	RKLGGDGSPTQVDVSQFGSFKEDTKMSISEGTVSDKSATPVDEGAEDT---YSHMEGVAS	1447
QY	524	VTEEVVA--NMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQES-LYPAA	580
Db	1448	VSTASVATSSFPPEPTTDD-VSPSLHAEVGS PHSTEVDDSLSVSVVQTPTTFQETEMSPSK	1506
QY	581	QLCP-----SFESEATPSPVLPDIVMEAPLNSAV-----P	611
Db	1507	EECPRMSISPPDFSPKTAKSRTPVQDHRSEQSSMSIEFGQESPEHSLAMDFS RQSPDHP	1566
QY	612	SAGASVIQ----PSSSPLEASSVNYESIKHE--PENPPPY-----EEAMSVS-LKVSG	657
Db	1567	TVGAGMLHITENGPTTEVDYSPSDIQDSSLSHKIPPTTEEPSYTDNDLSELISVSQVEASP	1626
QY	658	IKEEIKEPENINAALQETE-----APYISIIACDLIKE---TKLSAEP-----	696
Db	1627	STSSAHTPSQIASPLQEDTLSDVPPPRDMSLYASLASEKVQSLEGEKLSPKSDISPLTPR	1686
QY	697	-----APDFSDYSEMAK-----VEQPVPDHSELVEDS-----	723
Db	1687	ESSPTYSPGFSDSTSGAKESTAAYQTSSSPPIDAAAAEYPGRSSMLFDTMQHHLALSRD	1746
QY	724	-----SPDSEPVDLFSDD---SIPDVP----QKQD	746
Db	1747	LTTSSVEKDNGGKTPGDFNYAYQKPESTTESPDEEDYDYESHEKTIQAHDVGGYYYEKE	1806
QY	747	ETVML-----VKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKD	797



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      | :      | | : |      | || : | || |      : ::
Db      1807 RTIKSPCDSGYSYETIEKTTKTPEDGGYSCEITEKTTTRTPEEGGYSY-----EISEK 1858

QY      798 TLLPDEVS--TLSKKEKIPLQMEELSTAVYSNDD-----LFISKEA 836
      |   ||| | | | :      ::::|      :|      |   | :
Db      1859 TTRTPEVSGYTYEKTERRRLLDDISNGYDDTEDGGHTLGDCSYSYETTEKITSFPESES 1918

QY      837 QIRETETFSDDSSP-----IEIIDEFPTLISSKTDSEFSKLAREYT-----DL 877
      || | : ||      | ::      : | | : | ||      ||
Db      1919 YSYETTTKTTTRSPDTSAYCYETMEKITKTPQASTYSYETSDRCYTPERKSPSEARQDVDL 1978

QY      878 -----EVSH-KSEIANA---PDG----AGSLPCTELPHDLSLKNIQP-----KV 913
      | | | : : : | :      || | | | :      | :
Db      1979 CLVSSCEFKHPKTELSPSFNPNPLEWFAGEEPTESERPLTQSGGAPPPSGGKQQGRQC 2038

QY      914 EEKISFSDDFSKNKSATSKVLLLPDVSALGHTQAEIESIVKPKVLEKEAEKK-LPSD-- 970
      :| | | | | | | | :      | ||      | : | | : : | :
Db      2039 DETPPTSVSESAPSQTDSDV---PPETE-----ECPSITADANLSEDESEETIPTDKT 2088

QY      971 -----TEKEDRSPS-----AIFSADLGKTSVVDLLYWRDIKKTG 1004
      : || || |      : || | || | |
Db      2089 VTYKHMDPPPAPMQDRSPSPRHPDVMVDPEALAEQNLGKALKKDLKEKAKTKKPG 2145

```

# RESULT 15

## QRMSP1

microtubule-associated protein MAP1B - mouse

N;Alternate names: microtubule-associated protein MAP1(X); microtubule-associated protein MAP1.2; microtubule-associated protein MAP5

C;Species: Mus musculus (house mouse)

C;Date: 30-Sep-1991 #sequence\_revision 30-Sep-1991 #text\_change 01-Sep-2000

C;Accession: S07549; S44387; A33645

R;Noble, M.; Lewis, S.A.; Cowan, N.J.

J. Cell Biol. 109, 3367-3376, 1989

A;Title: The microtubule binding domain of microtubule-associated protein MAP1B contains a repeated sequence motif unrelated to that of MAP2 and tau.

A;Reference number: A33645; MUID:90094539; PMID:2480963

A;Accession: S07549

A;Molecule type: mRNA

A;Residues: 1-2464 <NOB>

A;Cross-references: EMBL:X51396; NID:g52999; PIDN:CAA35761.1; PID:g53000

R;Sanchez, C.; Padilla, R.; Paciucci, R.; Zabala, J.C.; Avila, J.  
Arch. Biochem. Biophys. 310, 428-432, 1994

A;Title: Binding of heat-shock protein 70 (hsp70) to tubulin.

A;Reference number: S44387; MUID:94234720; PMID:8179328

A;Accession: S44387

A;Status: preliminary

A;Molecule type: protein

A;Residues: 653-663, 'IC' <SAN>

C;Superfamily: microtubule-associated protein MAP1B

C;Keywords: microtubule binding; phosphoprotein; tandem repeat

F;589-786/Domain: microtubule binding #status experimental <MTB>

F;589-592, 639-642, 649-652, 655-658, 660-663, 668-671, 674-677, 679-682, 683-686, 687-690, 691-694, 695-698, 699-702, 708-711, 712-715, 716-719, 720-723, 727-730, 758-761, 764-767, 783-786/Region: 4-residue repeats (K/R-K-E/D-X)

F;1861-2064/Region: 17-residue repeats

F;91,116,351,888,1124,1153,1168,1208,1662,1877,1918,2003,2030,2054,2083/Binding site: phosphate (Ser) (covalent) #status predicted  
 F;147,969,1336,1562,1563,1702,1708,1990,2057,2063,2419/Binding site: phosphate (Thr) (covalent) #status predicted  
 F;1953/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 4.9%; Score 289; DB 1; Length 2464;  
 Best Local Similarity 19.8%; Pred. No. 0.0005;  
 Matches 262; Conservative 148; Mismatches 474; Indels 442; Gaps 55;

Qy	32	EDEEEEEEEEEDEDEDL-EELEVLERKPAAGLSAAPVPTAPAAGAPLMDFGNDFFVPPAP	90
		:           :     :       :	
Db	1009	EAEQSEEEGEEEDKAEDAREEGYEPDKTEAEDYVMAVADKAAEAGVTEEQYGY-----	1061
Qy	91	RGPLPAAPPV-APERQPSWDPSVSSSTVPAPSPLSAAVSPSKLPEDDEPPARPPPPPPA	149
		: :     :   :   :       :	
Db	1062	LGTSAKQPGIQSPSREPA--SSIHDETLPGGSESEATA-----SDEENREDQPEEFTA	1112
Qy	150	SVSPQAEFVWTPPAPAPAAPSTPAAPKRRGSSGAVVXXXXKIMDLKEQPGNTISAGQED	209
		: :         :   :	
Db	1113	TSGYTQSTIEISSEPTPMDEMSTP-----RDVMSDETNNNEETESPSQEF	1156
Qy	210	FPSVLLETAASXPSLSPLSAASEFK-----EHEYLGNLSTVLPTEGTLQENVSE	257
		: :   :     :   :     :   :	
Db	1157	VNITKYESSLYSQEYSKPAVASFNGLSEGSTDATDGKDYNASASTISPPSSMEEDKFSK	1216
Qy	258	AS-----KEVSEK-----AKTLLIDRDLTEFS	279
		: :   :   :       :   :	
Db	1217	SALRDAYCSEEKELKASAEIDIKDVSDERLSPAKSPSLSPSPSPPIEKTPLGERSV-NFS	1275
Qy	280	---ELEYSEMGSFSVSPKAESAVI---VANPRE---EIIVKNK-----	314
		:     :         :       : :	
Db	1276	LTPNEIKVSAEGEARSVSPGVQTQAVVEEHCASPEEKTLEVVSQSQSVTGSAGHTPYQSP	1335
Qy	315	-DEEEKLVSNILHXQQELPTALTCLVKEDEVVSSEKAKDSFNEKRVAVEAPMREEYADF	373
		: :   :   : :         :	
Db	1336	TDEKSSHLPTVEVSENAQAVPVSF-----EFSEAKDE-NER--ASLSPMDEPVPDS	1382
Qy	374	K-PFERVWE-----VKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSE	425
		:     :   :     :   :	
Db	1383	ESPVEKVLSPLRSPPLLGSSESPYEDFLSADSKVLGR-----RSESPFE	1425
Qy	426	SSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSENXT-----	478
		:   :   :	
Db	1426	GKNGKQGFPDRESPVSD-----LTSTGLYQDKQEEKSTGFIPIKEDFGPEKKTSDVETMS	1480
Qy	479	-----DEKKI-----EEKKAQIVTEKNTSTKTSNPFVAAQDSETD	514
		: :   :   :     :     :	
Db	1481	SQSALALDERKLGGDVSPTQIDVSQFGSFKEDTKMSISEGTVSDKSATP--VDEGVAEDT	1538
Qy	515	YVTTDNLTKVTEEVVA--NMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVM	572
		: :     :       : :   : :	
Db	1539	YSHMEGVASVSTASVATSSFFPEPTTDD-VSPSLHAEVGSPhSTEVDDSLSVSVVQTPTTF	1597
Qy	573	QES-LYPAAQLCP-----SFESEATPSPVLPDIVMEAPLNSAV--	610
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Qy 611 -----PSAGASVIQ-----PSSSPLEASSVNYESIKHE--PENPPPY-----EEAM 649  
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 Job time : 39.8322 secs

OM protein - protein search, using sw model

Run on: September 29, 2004, 18:16:15 ; Search time 126.45 Seconds  
(without alignments)  
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Title: US-09-830-972-29  
Perfect score: 5923  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1351062 seqs, 321799191 residues

Total number of hits satisfying chosen parameters: 1351062

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Published Applications\_AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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No.	Score	Match	Length	DB	ID	Description	

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2	5815	98.2	1192	9	US-09-972-599A-6	Sequence 6, Appli
3	5815	98.2	1192	14	US-10-060-036-71	Sequence 71, Appl
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5	5810	98.1	1192	9	US-09-893-348-23	Sequence 23, Appl
6	5810	98.1	1192	12	US-10-267-502-429	Sequence 429, App
7	5810	98.1	1192	16	US-10-327-213-9	Sequence 9, Appli
8	5810	98.1	1192	16	US-10-466-258-9	Sequence 9, Appli
9	5794	97.8	1192	12	US-10-408-967-7	Sequence 7, Appli
10	4296.5	72.5	1163	9	US-09-893-348-18	Sequence 18, Appl
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14	1495.5	25.2	373	9	US-09-893-348-24	Sequence 24, Appl
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16	1495.5	25.2	373	14	US-10-060-036-72	Sequence 72, Appl
17	1487.5	25.1	373	16	US-10-466-258-4	Sequence 4, Appli
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41	541.5	9.1	168	10	US-09-809-391-563	Sequence 563, App
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44	520	8.8	222	12	US-10-267-502-428	Sequence 428, App
45	513	8.7	241	12	US-10-660-946-3	Sequence 3, Appli

#### ALIGNMENTS

##### RESULT 1

US-09-758-140-6

; Sequence 6, Application US/09758140

; Patent No. US20020012965A1

; GENERAL INFORMATION:

; APPLICANT: Strittmatter, Stephen M.

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; TITLE OF INVENTION: No. US20020012965A1o Receptor-Mediated Blockade of
Axonal Growth
; FILE REFERENCE: 44574-5073-US
; CURRENT APPLICATION NUMBER: US/09/758,140
; CURRENT FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: US 60/175,707
; PRIOR FILING DATE: 2000-01-12
; PRIOR APPLICATION NUMBER: US 60/207,366
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,378
; PRIOR FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-758-140-6

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Query Match          98.2%; Score 5815; DB 9; Length 1192;
Best Local Similarity 97.2%; Pred. No. 6.1e-284;
Matches 1160; Conservative 4; Mismatches 13; Indels 16; Gaps 3;

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RESULT 2

US-09-972-599A-6

; Sequence 6, Application US/09972599A

; Patent No. US20020077295A1

; GENERAL INFORMATION:

; APPLICANT: STRITTMATTER, STEPHEN M.

; TITLE OF INVENTION: NOGO-RECEPTOR-MEDIATED BLOCKADE OF AXONAL GROWTH

; FILE REFERENCE: C077 CIP US

; CURRENT APPLICATION NUMBER: US/09/972,599A

; CURRENT FILING DATE: 2001-10-06

; PRIOR APPLICATION NUMBER: PCT/US01/01041  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: 09/758,140  
; PRIOR FILING DATE: 2001-01-12  
; PRIOR APPLICATION NUMBER: 60/236,378  
; PRIOR FILING DATE: 2000-09-29  
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; PRIOR FILING DATE: 2000-05-26  
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; PRIOR FILING DATE: 2000-01-12  
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; LENGTH: 1192  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-972-599A-6

Query Match 98.2%; Score 5815; DB 9; Length 1192;  
Best Local Similarity 97.2%; Pred. No. 6.1e-284;  
Matches 1160; Conservative 4; Mismatches 13; Indels 16; Gaps 3;

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 Db 1080 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFVLMWVFTYVGALFNGLT 1139  
 QY 1126 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1140 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192

RESULT 3

US-10-060-036-71

; Sequence 71, Application US/10060036

; Publication No. US20030073144A1

; GENERAL INFORMATION:

; APPLICANT: Benson, Darin R.

; APPLICANT: Kalos, Michael D.

; APPLICANT: Lodes, Michael J.

; APPLICANT: Persing, David H.

; APPLICANT: Hepler, William T.

; APPLICANT: Jiang, Yuqiu

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY  
; TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER  
; FILE REFERENCE: 210121.566  
; CURRENT APPLICATION NUMBER: US/10/060,036  
; CURRENT FILING DATE: 2002-01-30  
; NUMBER OF SEQ ID NOS: 4560  
; SOFTWARE: FastSEQ for Windows Version 4.0  
; SEQ ID NO 71  
; LENGTH: 1192  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-060-036-71

Query Match 98.2%; Score 5815; DB 14; Length 1192;  
Best Local Similarity 97.2%; Pred. No. 6.1e-284;  
Matches 1160; Conservative 4; Mismatches 13; Indels 16; Gaps 3;

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Qy      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
          |||
Db      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60

Qy     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSVSTVPAP 120
          |||
Db     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSVSTVPAP 120

Qy    121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180
          |||
Db    121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180

Qy    181 SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP 226
          |||:      |:      : |||
Db    181 SSGSVDETFLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP 240

Qy    227 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTFSELEYSEM 286
          |||
Db    241 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTFSELEYSEM 300

Qy    287 GSSFVSVPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTCLKVKEDEVV 346
          |||
Db    301 GSSFVSVPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHNQQELPTALTCLKVKEDEVV 360

Qy    347 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 406
          |||
Db    361 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 420

Qy    407 DKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF 466
          |||
Db    421 DKKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF 480

Qy    467 PLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTQVTE 526
          |||
Db    481 PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTQVTE 540

Qy    527 EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF 586
          |||
Db    541 EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF 600
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Qy 587 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE 646  
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 Db 601 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE 660  
 Qy 647 EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSE 705  
 ||||||| ||||||||||||||||||||||||||||||||||||||||||||  
 Db 661 EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSE 720  
 Qy 706 MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVM LVKESLTETSFESMI 765  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 721 MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVM LVKESLTETSFESMI 780  
 Qy 766 EYENKEKLSALPPEGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 825  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 781 EYENKEKLSALPPEGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 840  
 Qy 826 SNDDLFI SKEAQIRETETFTSDSSPIEIIDEFPTLISSKTD SFSKLAREYTDLEVSHKSEI 885  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 841 SNDDLFI SKEAQIRETETFTSDSSPIEIIDEFPTLISSKTD SFSKLAREYTDLEVSHKSEI 900  
 Qy 886 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFS KNGSATS KVVLLLPPDV SALGH 945  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 901 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFS KNGSATS KVVLLLPPDV SALA- 959  
 Qy 946 TQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIF SADLGKTSVVDLLYWRDIKKTGV 1005  
 |||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||  
 Db 960 TQAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIF SAE LSKTSVVDLLYWRDIKKTGV 1019  
 Qy 1006 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRAYLES 1065  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1020 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRAYLES 1079  
 Qy 1066 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVD SLKFAVLMWVFTYVGALFNGLT 1125  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1080 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVD SLKFAVLMWVFTYVGALFNGLT 1139  
 Qy 1126 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQA KIPGLKRKAE 1178  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1140 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQA KIPGLKRKAE 1192

RESULT 4

US-09-789-386-2

; Sequence 2, Application US/09789386  
 ; Patent No. US20020010324A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: MICHALOVICH, DAVID  
 ; APPLICANT: PRINJHA, RABINDER KUMAR  
 ; TITLE OF INVENTION: NOVEL COMPOUNDS  
 ; FILE REFERENCE: GP-30165-C1  
 ; CURRENT APPLICATION NUMBER: US/09/789,386  
 ; CURRENT FILING DATE: 2001-02-21  
 ; PRIOR APPLICATION NUMBER: U.K. 9916898.1  
 ; PRIOR FILING DATE: 1999-07-19  
 ; PRIOR APPLICATION NUMBER: U.K. 9816024.5  
 ; PRIOR FILING DATE: 1998-07-22  
 ; PRIOR APPLICATION NUMBER: US 09/359,208

; PRIOR FILING DATE: 1999-07-22  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: FastSEQ for Windows Version 3.0  
; SEQ ID NO 2  
; LENGTH: 1192  
; TYPE: PRT  
; ORGANISM: HOMO SAPIENS  
US-09-789-386-2

Query Match 98.1%; Score 5810; DB 9; Length 1192;  
Best Local Similarity 97.2%; Pred. No. 1.1e-283;  
Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;

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Qy      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
      |||
Db      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60

Qy     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSVSTVPAP 120
      |||
Db     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSVSTVPAP 120

Qy    121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180
      |||
Db    121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180

Qy    181 SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLS 226
      |||:
Db    181 SSGSVDETLEFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLS 240

Qy    227 LSAASFKEHEYLGNLSTVLPTTEGLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 286
      |||
Db    241 LSAASFKEHEYLGNLSTVLPTTEGLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 300

Qy    287 GSSFSVSPKAESAVIVANPREEIIIVKNKDEEEKLVSNILHXQQELPTALTCLVKEDEVV 346
      |||
Db    301 GSSFSVSPKAESAVIVANPREEIIIVKNKDEEEKLVSNILHNQQELPTALTCLVKEDEVV 360

Qy    347 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 406
      |||
Db    361 SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV 420

Qy    407 DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF 466
      |||
Db    421 DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF 480

Qy    467 PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTQVTE 526
      |||
Db    481 PLLGDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTQVTE 540

Qy    527 EVVANMPEGLTPDLVQACESELNEVTGKIAIYETKMDLVQTSSEVMQESLYPAAQLCPSF 586
      |||
Db    541 EVVANMPEGLTPDLVQACESELNEVTGKIAIYETKMDLVQTSSEVMQESLYPAAQLCPSF 600

Qy    587 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE 646
      |||
Db    601 EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYE 660
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QY 647 EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSE 705  
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 Db 661 EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSE 720  
 QY 706 MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLKESLTETSFESMI 765  
 ||||| |||||  
 Db 721 MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLKESLTETSFESMI 780  
 QY 766 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 825  
 ||||| |||||  
 Db 781 EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY 840  
 QY 826 SNDDLFIKSEAQIRETETFSDDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI 885  
 ||||| |||||  
 Db 841 SNDDLFIKSEAQIRETETFSDDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI 900  
 QY 886 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATSQVLLLPDVSALGH 945  
 ||||| |||||  
 Db 901 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATSQVLLLPDVSALA- 959  
 QY 946 TQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSAADLGKTSVVDLLYWRDIKKTGV 1005  
 ||||| |||||:| |||||  
 Db 960 TQAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGV 1019  
 QY 1006 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES 1065  
 ||||| |||||  
 Db 1020 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES 1079  
 QY 1066 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFVLMWVFTYVGALFNGLT 1125  
 ||||| |||||  
 Db 1080 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFVLMWVFTYVGALFNGLT 1139  
 QY 1126 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178  
 ||||| |||||  
 Db 1140 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192

RESULT 5

US-09-893-348-23

; Sequence 23, Application US/09893348

; Patent No. US20020072493A1

; GENERAL INFORMATION:

; APPLICANT: EISENBACH-SCHWARTZ, Michal

; APPLICANT: COHEN, Irun R.

; APPLICANT: BESERMAN, Pierre

; APPLICANT: MOSONEGO, Alon

; APPLICANT: MOALEM, Gila

; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES

; FILE REFERENCE: EIS-SCHWARTZ=2A

; CURRENT APPLICATION NUMBER: US/09/893,348

; CURRENT FILING DATE: 2001-06-28

; PRIOR APPLICATION NUMBER: US 09/314,161

; PRIOR FILING DATE: 1999-05-19

; PRIOR APPLICATION NUMBER: US 09/218,277

; PRIOR FILING DATE: 1998-12-22

; PRIOR APPLICATION NUMBER: PCT/US98/14715

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; PRIOR FILING DATE: 1998-07-21
; PRIOR APPLICATION NUMBER: IL 124500
; PRIOR FILING DATE: 1998-05-19
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
;   LENGTH: 1192
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-893-348-23
```

Query Match 98.1%; Score 5810; DB 9; Length 1192;  
Best Local Similarity 97.2%; Pred. No. 1.1e-283;  
Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;

Qy	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Db	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVPSSTVPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVPSSTVPAP	120
Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Qy	181	SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP	226
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP	240
Qy	227	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	286
Db	241	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	287	GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTCLKVKEDEVV	346
Db	301	GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHNQQELPTALTCLKVKEDEVV	360
Qy	347	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	406
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	407	DKKCFADSLEQTNHEKDSSESNDDTSFSPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	466
Db	421	DKKCFADSLEQTNHEKDSSESNDDTSFSPSTPEGIKDRPGAYITCAPFNPAATESIATNIF	480
Qy	467	PLLEDPTSENXTDEKKIEEKKQAIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTE	526
Db	481	PLLGDPSTENKTDEKKIEEKKQAIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTE	540
Qy	527	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	586
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	587	ESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	646

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; Sequence 429, Application US/10267502
; Publication No. US20040071700A1
; GENERAL INFORMATION:
; APPLICANT: Kim, Jaeseob
; APPLICANT: Galant, Ron
; TITLE OF INVENTION: Obesity Linked Genes
; FILE REFERENCE: LSD-07416
; CURRENT APPLICATION NUMBER: US/10/267,502
; CURRENT FILING DATE: 2003-01-27
; NUMBER OF SEQ ID NOS: 439
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 429
; LENGTH: 1192
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-267-502-429
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Qy	766	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	825
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	826	SNDDLFIKSEAQIRETETFSDDSSPIEIIDEFPTLISSKTDSEFSKLAREYTDLEVSHKSEI	885
Db	841	SNDDLFIKSEAQIRETETFSDDSSPIEIIDEFPTLISSKTDSEFSKLAREYTDLEVSHKSEI	900
Qy	886	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSQVLLLPDVSALGH	945
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSQVLLLPDVSALA-	959
Qy	946	TQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSAADLGKTSVVDLLYWRDIKKTGV	1005
Db	960	TQAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGV	1019
Qy	1006	VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES	1065
Db	1020	VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES	1079
Qy	1066	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT	1125
Db	1080	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT	1139
Qy	1126	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1178
Db	1140	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1192

RESULT 7

US-10-327-213-9

; Sequence 9, Application US/10327213

; Publication No. US20040121341A1

; GENERAL INFORMATION:

; APPLICANT: FILBIN, MARIE T.

; APPLICANT: DOMENICONI, MARCO

; APPLICANT: CAO, ZIXUAN

; TITLE OF INVENTION: INHIBITORS OF MYELIN-ASSOCIATED GLYCOPROTEIN (MAG)

; TITLE OF INVENTION: ACTIVITY FOR REGULATING NEURAL GROWTH AND REGENERATION

; FILE REFERENCE: CUNY/003

; CURRENT APPLICATION NUMBER: US/10/327,213

; CURRENT FILING DATE: 2002-12-20

; NUMBER OF SEQ ID NOS: 43

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 9

; LENGTH: 1192

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-327-213-9

Query Match 98.1%; Score 5810; DB 16; Length 1192;

Best Local Similarity 97.2%; Pred. No. 1.1e-283;

Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;

Qy	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Db	1	MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60

Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDFSPVSSTVPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDFSPVSSTVPAP	120
Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKRRG	180
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKRRG	180
Qy	181	SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP	226
		:   :	
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP	240
Qy	227	LSAASFKEHEYLGNLSTVLPTTEGLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	286
Db	241	LSAASFKEHEYLGNLSTVLPTTEGLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	287	GSSFVSVPKAESAVIVANPREEIIIVKNKDEEEKLVSNILHXQQELPTALTCLVKEDEVV	346
Db	301	GSSFVSVPKAESAVIVANPREEIIIVKNKDEEEKLVSNILHNQQELPTALTCLVKEDEVV	360
Qy	347	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	406
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	407	DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	466
Db	421	DKKCFADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF	480
Qy	467	PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTE	526
Db	481	PLLDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE	540
Qy	527	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	586
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	587	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	646
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	647	EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFS DYSE	705
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFS DYSE	720
Qy	706	MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFESMI	765
Db	721	MAKVEQPVPDHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFESMI	780
Qy	766	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	825
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	826	SNDDLFIKSEAQIRETETFS DSSPIEIIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI	885
Db	841	SNDDLFIKSEAQIRETETFS DSSPIEIIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI	900

Qy 886 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPDVSALGH 945  
 |||  
 Db 901 ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPDVSALA- 959  
 Qy 946 TQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGV 1005  
 |||:|  
 Db 960 TQAEIESIVKPKVLVKEAEKKLPSDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGV 1019  
 Qy 1006 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES 1065  
 |||  
 Db 1020 VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES 1079  
 Qy 1066 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFVLMWVFTYVGALFNGLT 1125  
 |||  
 Db 1080 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFVLMWVFTYVGALFNGLT 1139  
 Qy 1126 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178  
 |||  
 Db 1140 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192

RESULT 8

US-10-466-258-9

; Sequence 9, Application US/10466258  
 ; Publication No. US20040132096A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: GLAXO GROUP LIMITED  
 ; TITLE OF INVENTION: ASSAY  
 ; FILE REFERENCE: P80966 GCW  
 ; CURRENT APPLICATION NUMBER: US/10/466,258  
 ; CURRENT FILING DATE: 2003-07-15  
 ; NUMBER OF SEQ ID NOS: 13  
 ; SOFTWARE: PatentIn version 3.0  
 ; SEQ ID NO 9  
 ; LENGTH: 1192  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-466-258-9

Query Match 98.1%; Score 5810; DB 16; Length 1192;  
 Best Local Similarity 97.2%; Pred. No. 1.1e-283;  
 Matches 1159; Conservative 4; Mismatches 14; Indels 16; Gaps 3;

Qy 1 MEDLDQSPLVSSSDSPPRQPAPFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60  
 |||  
 Db 1 MEDLDQSPLVSSSDSPPRQPAPFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60  
 Qy 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSSTVPAP 120  
 |||  
 Db 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSSTVPAP 120  
 Qy 121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVWTPPAPAPAAPSTPAAPKRRG 180  
 |||  
 Db 121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVWTPPAPAPAAPSTPAAPKRRG 180  
 Qy 181 SSGA-----VXXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSLSP 226  
 |||:|:|

Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLS	240
Qy	227	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	286
Db	241	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	287	GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNILHXQQELPTALTCLKVKEDEVV	346
Db	301	GSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNILHNNQQELPTALTCLKVKEDEVV	360
Qy	347	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	406
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	407	DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	466
Db	421	DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF	480
Qy	467	PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTE	526
Db	481	PLLGDPPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTE	540
Qy	527	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	586
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	587	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	646
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	647	EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFS DYSE	705
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFS DYSE	720
Qy	706	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETS FESMI	765
Db	721	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETS FESMI	780
Qy	766	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	825
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	826	SNDDLFI SKEAQIRETETFS DSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI	885
Db	841	SNDDLFI SKEAQIRETETFS DSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEI	900
Qy	886	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFS KNGSATS KVVLLLPDVSALGH	945
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFS KNGSATS KVVLLLPDVSALA-	959
Qy	946	TQAEIESIVKPKVLEKEAEKKLPSTEKEDRSPSAIFSA DLGKTSVVDLLYWRDIKKTGV	1005
Db	960	TQAEIESIVKPKVLVKEAEKKLPSTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGV	1019
Qy	1006	VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRAYLES	1065
Db	1020	VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRAYLES	1079

Qy 1066 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFVILMWVFTTYVGALFNGLT 1125  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1080 EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDSLKFVILMWVFTTYVGALFNGLT 1139  
 Qy 1126 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1140 LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1192

RESULT 9

US-10-408-967-7

; Sequence 7, Application US/10408967  
 ; Publication No. US20040063161A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Pharmacia & Upjohn Company  
 ; APPLICANT: Yan, Riqiang  
 ; APPLICANT: Lu, Yifeng  
 ; TITLE OF INVENTION: Compositions and Methods of Treating Alzheimer's Disease  
 ; FILE REFERENCE: 00925  
 ; CURRENT APPLICATION NUMBER: US/10/408,967  
 ; CURRENT FILING DATE: 2003-04-08  
 ; NUMBER OF SEQ ID NOS: 9  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 7  
 ; LENGTH: 1192  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-408-967-7

Query Match 97.8%; Score 5794; DB 12; Length 1192;  
 Best Local Similarity 97.0%; Pred. No. 6.9e-283;  
 Matches 1157; Conservative 4; Mismatches 16; Indels 16; Gaps 3;

Qy 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEDEDEDLEELEVLERKPA 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEDEDEDLEELEVLERKPA 60  
 Qy 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120  
 Qy 121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180  
 Qy 181 SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP 226  
 |||: | : : ||||||||||||||||||||||||||||||||  
 Db 181 SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP 240  
 Qy 227 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 286  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 241 LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM 300  
 Qy 287 GSSFSVSPKAESAVIVANPREEIIIVKNKDEEEKLVSNILHXQQELPTALTCLVKEDEVV 346  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 301 GSSFSVSPKAESAVIVANPREEIIIVKNKDEEEKLVSNILHNQQELPTALTCLVKEDEVV 360

Qy	347	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	406
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	407	DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	466
Db	421	DKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRPGAYITCAPFNPAATESIATNIF	480
Qy	467	PLLEDPTSSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTE	526
Db	481	PLLGDPSTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE	540
Qy	527	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	586
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	587	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	646
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	647	EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFS DYSE	705
Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFS DYSE	720
Qy	706	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETS FESMI	765
Db	721	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETS FESMI	780
Qy	766	EYENKEKLSALPPEGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	825
Db	781	EYENKEKLSALPPEGKPYLESFKLSLINTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	826	SNDDLFI SKEAQIRETETFS DSSPIEII DEFPTLISSKTDSFSKLAREYTDLEVSHKSEI	885
Db	841	SNDDLFI SKEAQIRETETFS DSSPIEII DEFPTLISSKTDSFSKLAREYTDLEVSHKSEI	900
Qy	886	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATS KVL LPPDV SALGH	945
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATS KVL LPPDV SALA-	959
Qy	946	TQAEIESIVKPKVLEKEAEKKLPSTEKEDRSPSAIF SADLGKTSVVDLLYWRDIKKTGV	1005
Db	960	TQAEIESIVKPKVLVKEAEKKLPSTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGV	1019
Qy	1006	VFGASLFL LLSLT VFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGH PFRAYLES	1065
Db	1020	VFGASLFL LLSLT VFSIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGH PFPAYLES	1079
Qy	1066	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT	1125
Db	1080	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT	1139
Qy	1126	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1178
Db	1140	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1192

RESULT 10

US-09-893-348-18

; Sequence 18, Application US/09893348

; Patent No. US20020072493A1

; GENERAL INFORMATION:

; APPLICANT: EISENBACH-SCHWARTZ, Michal

; APPLICANT: COHEN, Irun R.

; APPLICANT: BESERMAN, Pierre

; APPLICANT: MOSONEGO, Alon

; APPLICANT: MOALEM, Gila

; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES

; FILE REFERENCE: EIS-SCHWARTZ=2A

; CURRENT APPLICATION NUMBER: US/09/893,348

; CURRENT FILING DATE: 2001-06-28

; PRIOR APPLICATION NUMBER: US 09/314,161

; PRIOR FILING DATE: 1999-05-19

; PRIOR APPLICATION NUMBER: US 09/218,277

; PRIOR FILING DATE: 1998-12-22

; PRIOR APPLICATION NUMBER: PCT/US98/14715

; PRIOR FILING DATE: 1998-07-21

; PRIOR APPLICATION NUMBER: IL 124500

; PRIOR FILING DATE: 1998-05-19

; NUMBER OF SEQ ID NOS: 29

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 18

; LENGTH: 1163

; TYPE: PRT

; ORGANISM: Rattus norvegicus

US-09-893-348-18

Query Match 72.5%; Score 4296.5; DB 9; Length 1163;

Best Local Similarity 74.0%; Pred. No. 1.3e-207;

Matches 885; Conservative 104; Mismatches 156; Indels 51; Gaps 19;

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Qy      1 MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEE-EEEEEEEEDEDEDLEELEVLERK 58
      |||:||| ||||| ||||| ||||| ||||| ||||| |||||:|||:||| ||||| |||||
Db      1 MEDIDQSSLVSSSTDSPPRPPPAFKYQFVTEPEDEDEEEEEDEEDEDLEELEVLERK 60

Qy     59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVP 118
      ||||| || || ||| |||:||| :| ||||| ||||| |||||:||| :| :| |
Db     61 PAAGLSAAAVP--PAAAAPLLDFSSDSVPAPRGPLPAAPPAAPERQPSWERSPAA---P 115

Qy    119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKR 178
      ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db    116 APSLPAAAVLPSKLPEDDEPPARPPPPPPAGASPLAE-----PAAPPSTPAAPKR 166

Qy    179 RGSSG-----AVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSSL 224
      ||| : ||||| |||||:|||:||| ||||| ||||| ||||| ||||| |||||
Db    167 RGSGSVDETLFALPAASEVIPSSAEKIMDLMEQPGNTVSSGQEDFPSVLLETAASLPSSL 226

Qy    225 SPLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYS 284
      |||| ||||| ||||| | :|||:||| ::||||| :|:| ::||| ||||| |||||
Db    227 SPLSTVSFKEHGYLGNLSAVSSSEGTIEETLNEASKELPERATNPFVNRDLAEFSELEYS 286

Qy    285 EMGSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNILHXQQELPTALTCLKVKEDE 344

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Db	287	EMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG-----KEDR	340
Qy	345	VVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNLE	403
Db	341	VVSPEKTMDIFNEMQMSVVPVREEYADFKPFEQAWVEVKDTEGSRDVLAA-----RANVE	396
Qy	404	SKVDKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIAT	463
Db	397	SKVDRKCLEDSEQKSLGKDSEGRNEDASFPSTPEPVKDSRAYITCASFT-SATESTTA	455
Qy	464	NIFPLLEDPTSENXTDEKKIEEKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTK	523
Db	456	NTFPLLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFVAVQDSEADYVTDTLSK	514
Qy	524	VTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLC	583
Db	515	VTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQLC	574
Qy	584	PSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEA-SSVNYESIKHEPENP	642
Db	575	PSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPVSYDSIKLEPENP	634
Qy	643	PPYEEAMSVSLKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSD	702
Db	635	PPYEEAMNVALKALGTKEGIKEPESFNAAVQETEAPYISACDLIKETKLSTEPSPDFSN	694
Qy	703	YSEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVMVLKESLTETSFE	762
Db	695	YSEIAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVS-E	753
Qy	763	SMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELST	822
Db	754	TVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLQMEEFNT	811
Qy	823	AVYSNDDLFISKEAQIRETETFSDDSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHK	882
Db	812	AIYSNDDLLSSKEDKIKESETFSDDSPIEIIDEFPTFVSAKDDS-PKLAKEYTDLEVSDK	870
Qy	883	SEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATSKVLLLPPDVSA	942
Db	871	SEIANIQSGADSLPCLLPCLDSFKNIYPK--DEVHVSDEFSENRSSVSKASISPSNVSA	928
Qy	943	LGHTQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKK	1002
Db	929	L-EPQTEMGSIKSKSLTKEAEKKLPDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKK	987
Qy	1003	TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAY	1062
Db	988	TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAY	1047
Qy	1063	LESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFN	1122
Db	1048	LESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFN	1107
Qy	1123	GLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1178







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; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GP-30165-C1
; CURRENT APPLICATION NUMBER: US/09/789,386
; CURRENT FILING DATE: 2001-02-21
; PRIOR APPLICATION NUMBER: U.K. 9916898.1
; PRIOR FILING DATE: 1999-07-19
; PRIOR APPLICATION NUMBER: U.K. 9816024.5
; PRIOR FILING DATE: 1998-07-22
; PRIOR APPLICATION NUMBER: US 09/359,208
; PRIOR FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 373
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-789-386-6
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Query Match          25.2%; Score 1495.5; DB 9; Length 373;
Best Local Similarity 31.6%; Pred. No. 2.1e-67;
Matches 372; Conservative 1; Mismatches 0; Indels 805; Gaps 1;
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Qy      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60
        |||
Db      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60

Qy     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120
        |||
Db     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP 120

Qy    121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKRRG 180
        |||
Db    121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKRRG 180

Qy    181 SSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAAAFKEHEYLGN 240
        |||:|
Db    181 SSGSV----- 185

Qy    241 LSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFVSFVSPKAESAV 300
Db    186 ----- 185

Qy    301 IVANPREEIIVKNKDEEEKLVSNNI LHXQQELPTALT KLKVEDEVVSSEKAKDSFNEKRV 360
Db    186 ----- 185

Qy    361 AVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNH 420
Db    186 ----- 185

Qy    421 EKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSENXTDE 480
Db    186 ----- 185

Qy    481 KKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVT'DNLT'KVTEEVVANMPEGLTPDL 540
Db    186 ----- 185
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Qy	541	VQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPDI	600
Db	186	-----	185
Qy	601	VMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSGIKE	660
Db	186	-----	185
Qy	661	EIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELV	720
Db	186	-----	185
Qy	721	EDSSPDSEPVDLFDSDSIPDVPQKQDETVMVLVKESLTETSFESMIEYENKEKLSALPPEG	780
Db	186	-----	185
Qy	781	GKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFISKEAQIRE	840
Db	186	-----	185
Qy	841	TETFSDDSSPIEIIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTEL	900
Db	186	-----	185
Qy	901	PHDLSLKNIQPKVEEKISFSDDFSNGSATSKVLLLPDVSALGHTQAEIESIVKPKVLE	960
Db	186	-----	185
Qy	961	KEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVF	1020
Db	186	-----VVDLLYWRDIKKTGVVFGASLFLLLSLTVF	215
Qy	1021	SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS	1080
Db	216	SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS	275
Qy	1081	ALGHVNCTIKELRRLFLVDDLVDLSLKFVLMWVFTYVGALFNGLTLLILALISLFSVPVI	1140
Db	276	ALGHVNCTIKELRRLFLVDDLVDLSLKFVLMWVFTYVGALFNGLTLLILALISLFSVPVI	335
Qy	1141	YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1178
Db	336	YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	373

RESULT 13

US-09-765-205-6

; Sequence 6, Application US/09765205

; Patent No. US20020034800A1

; GENERAL INFORMATION:

; APPLICANT: Cao, Li

; TITLE OF INVENTION: BONE MARROW SECRETED PROTEINS AND POLYNUCLEOTIDES

; FILE REFERENCE: 1458.004/200130.449

; CURRENT APPLICATION NUMBER: US/09/765,205

; CURRENT FILING DATE: 2001-01-17

; PRIOR APPLICATION NUMBER: US/09/212,440

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; PRIOR FILING DATE: 1998-12-16
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 6
; LENGTH: 373
; TYPE: PRT
; ORGANISM: human
US-09-765-205-6
```

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Query Match          25.2%; Score 1495.5; DB 9; Length 373;
Best Local Similarity 31.6%; Pred. No. 2.1e-67;
Matches 372; Conservative 1; Mismatches 0; Indels 805; Gaps 1;
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Qy      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEDEDEDLEELEVLERKPA 60
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Db      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEDEDEDLEELEVLERKPA 60

Qy     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVVSSTVPAP 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVVSSTVPAP 120

Qy    121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180

Qy    181 SSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAA SFKEHEYLGN 240
        |||:|
Db    181 SSGSV----- 185

Qy    241 LSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSVSPKAESAV 300
Db    186 ----- 185

Qy    301 IVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTCLVKEDEVVSSEKAKDSFNEKRV 360
Db    186 ----- 185

Qy    361 AVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNH 420
Db    186 ----- 185

Qy    421 EKDSSESSNDDTSFSPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSENXTDE 480
Db    186 ----- 185

Qy    481 KKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTEEVVANMPEGLTPDL 540
Db    186 ----- 185

Qy    541 VQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFESEATPSPVLPDI 600
Db    186 ----- 185

Qy    601 VMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSGIKE 660
Db    186 ----- 185
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Qy 661 EIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSEMAKVEQPVPDHSELV 720

Db 186 ----- 185

Qy 721 EDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETSFESMIEYENKEKLSALPPEG 780

Db 186 ----- 185

Qy 781 GKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDL FISK EAQIRE 840

Db 186 ----- 185

Qy 841 TETFS DSSPIEII DEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTEL 900

Db 186 ----- 185

Qy 901 PHDLSLKNIQPKVEEKISFSDDFS KNGSATS KVVLLLPDVSALGHTQAEIESIVKPKVLE 960

Db 186 ----- 185

Qy 961 KEAEKKLP SDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASL FLLLSLTVF 1020  
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Db 186 -----VVDLLYWRDIKKTGVVFGASL FLLLSLTVF 215

Qy 1021 SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS 1080  
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Db 216 SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS 275

Qy 1081 ALGHVNCTIKELRRLFLVDDLVD SLKFVLMWVFTYV GALFNGLTLLILALISLFSVPVI 1140  
 ||||||||||||||||||

Db 276 ALGHVNCTIKELRRLFLVDDLVD SLKFVLMWVFTYV GALFNGLTLLILALISLFSVPVI 335

Qy 1141 YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178  
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Db 336 YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 373

RESULT 14

US-09-893-348-24

; Sequence 24, Application US/09893348

; Patent No. US20020072493A1

; GENERAL INFORMATION:

; APPLICANT: EISENBACH-SCHWARTZ, Michal

; APPLICANT: COHEN, Irun R.

; APPLICANT: BESERMAN, Pierre

; APPLICANT: MOSONEGO, Alon

; APPLICANT: MOALEM, Gila

; TITLE OF INVENTION: ACTIVATED T-CELLS, NERVOUS SYSTEM-SPECIFIC ANTIGENS AND THEIR USES

; FILE REFERENCE: EIS-SCHWARTZ=2A

; CURRENT APPLICATION NUMBER: US/09/893,348

; CURRENT FILING DATE: 2001-06-28

; PRIOR APPLICATION NUMBER: US 09/314,161

; PRIOR FILING DATE: 1999-05-19

; PRIOR APPLICATION NUMBER: US 09/218,277

; PRIOR FILING DATE: 1998-12-22

; PRIOR APPLICATION NUMBER: PCT/US98/14715

; PRIOR FILING DATE: 1998-07-21  
; PRIOR APPLICATION NUMBER: IL 124500  
; PRIOR FILING DATE: 1998-05-19  
; NUMBER OF SEQ ID NOS: 29  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 24  
; LENGTH: 373  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-893-348-24

Query Match 25.2%; Score 1495.5; DB 9; Length 373;  
Best Local Similarity 31.6%; Pred. No. 2.1e-67;  
Matches 372; Conservative 1; Mismatches 0; Indels 805; Gaps 1;

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Qy      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEDEDEDLEELEVLERKPA 60
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Db      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEDEDEDLEELEVLERKPA 60

Qy     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSSVTPAP 120
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Db     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSSVTPAP 120

Qy    121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180
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Db    121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180

Qy    181 SSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAAAFKEHEYLGN 240
          |||:|
Db    181 SSGSV----- 185

Qy    241 LSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSVSPKAESAV 300
Db    186 ----- 185

Qy    301 IVANPREEIIVKNKDEEEKLVSNILHXQQELPTALTCLVKEDEVVSSEKAKDSFNEKRV 360
Db    186 ----- 185

Qy    361 AVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNH 420
Db    186 ----- 185

Qy    421 EKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSENXTDE 480
Db    186 ----- 185

Qy    481 KKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTQVTEEVVANMPEGLTPDL 540
Db    186 ----- 185

Qy    541 VQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPDI 600
Db    186 ----- 185

Qy    601 VMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSGIKE 660
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Db	186	-----	185
Qy	661	EIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELV	720
Db	186	-----	185
Qy	721	EDSSPDSEPVDLFSDDSIIPDVPQKQDETVMVLVKESLTETSFESMIEYENKEKLSALPPEG	780
Db	186	-----	185
Qy	781	GKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFIKSEAQIRE	840
Db	186	-----	185
Qy	841	TETFSDDSSPIEIIIDEFPTLISSKTDSDFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTEL	900
Db	186	-----	185
Qy	901	PHDLSLKNIQPKVEEKISFSDDFSNGSATSQVLLLPDVSALGHTQAEIESIVKPKVLE	960
Db	186	-----	185
Qy	961	KEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASLFLLSLTVF	1020
Db	186	-----VVDLLYWRDIKKTGVVFGASLFLLSLTVF	215
Qy	1021	SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS	1080
Db	216	SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS	275
Qy	1081	ALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI	1140
Db	276	ALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI	335
Qy	1141	YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1178
Db	336	YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	373

RESULT 15

US-10-408-967-8

; Sequence 8, Application US/10408967

; Publication No. US20040063161A1

; GENERAL INFORMATION:

; APPLICANT: Pharmacia & Upjohn Company

; APPLICANT: Yan, Riqiang

; APPLICANT: Lu, Yifeng

; TITLE OF INVENTION: Compositions and Methods of Treating Alzheimer's Disease

; FILE REFERENCE: 00925

; CURRENT APPLICATION NUMBER: US/10/408,967

; CURRENT FILING DATE: 2003-04-08

; NUMBER OF SEQ ID NOS: 9

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 8

; LENGTH: 373

; TYPE: PRT

; ORGANISM: Homo sapiens



US-10-408-967-8

Query Match 25.2%; Score 1495.5; DB 12; Length 373;  
Best Local Similarity 31.6%; Pred. No. 2.1e-67;  
Matches 372; Conservative 1; Mismatches 0; Indels 805; Gaps 1;

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Qy      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEDEDEDLEELEVLERKPA 60
      |||
Db      1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEDEDEDLEELEVLERKPA 60

Qy     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120
      |||
Db     61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSTVPAP 120

Qy    121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180
      |||
Db    121 SPLSAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG 180

Qy    181 SSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAASFKEHEYLG 240
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Db    181 SSGSV----- 185

Qy    241 LSTVLPTTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSVSPKAESAV 300
      |
Db    186 ----- 185

Qy    301 IVANPREEIIVKNKDEEEKLVSNILHXQQELPTALTCLVKEDEVSSSEKAKDSFNEKRV 360
      |
Db    186 ----- 185

Qy    361 AVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDDKKCFADSLEQTNH 420
      |
Db    186 ----- 185

Qy    421 EKDSSESNDDTSFSTPEGIKDRSGAYITCAPFNPAATESIATNIFLLEDPTSENXTDE 480
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Db    186 ----- 185

Qy    481 KKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTEEVVANMPEGLTPDL 540
      |
Db    186 ----- 185

Qy    541 VQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPDI 600
      |
Db    186 ----- 185

Qy    601 VMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSGIKE 660
      |
Db    186 ----- 185

Qy    661 EIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELV 720
      |
Db    186 ----- 185

Qy    721 EDSSPDSEPVDLFSDDSIIPDVPQKQDETVMVLKESLTETSFESMIEYENKEKLSALPPEG 780
      |
Db    186 ----- 185
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Qy 781 GKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFI SKEAQIRE 840

Db 186 ----- 185

Qy 841 TETFS DSSPIEIIIDEFPTLISSKTD SFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTEL 900

Db 186 ----- 185

Qy 901 PHDLSLKNIQPKVEEKISFSDDFSKNGSATS KVL LPPDV SALGHTQAEIESIVKPKVLE 960

Db 186 ----- 185

Qy 961 KEAEKKLP SDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASL FLLLSLTVF 1020

Db 186 -----VVDLLYWRDIKKTGVVFGASL FLLLSLTVF 215

Qy 1021 SIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRAYLESEVAISEELVQKYSNS 1080

Db 216 SIVSVTAYIALALLSVTISFRIYKGV IQAIQKSDEGHPFRAYLESEVAISEELVQKYSNS 275

Qy 1081 ALGHVNCTIKELRRLFLVDDLVD SLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI 1140

Db 276 ALGHVNCTIKELRRLFLVDDLVD SLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI 335

Qy 1141 YERHQAQIDHYLGLANKNVKDAMAKIQA KIPGLKRKAE 1178

Db 336 YERHQAQIDHYLGLANKNVKDAMAKIQA KIPGLKRKAE 373

Search completed: September 29, 2004, 18:48:18  
 Job time : 132.45 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 29, 2004, 18:06:43 ; Search time 92.6748 Seconds  
(without alignments)  
4010.587 Million cell updates/sec

Title: US-09-830-972-29  
Perfect score: 5923  
Sequence: 1 MEDLDQSPLVSSSDSPRPQ.....VKDAMAKIQAKIPGLKRKAE 1178

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SPTREMBL\_25:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_rodent:\*  
12: sp\_virus:\*  
13: sp\_vertibrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match Length DB	ID	Description
No.					

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1	4851	81.9	986	4	Q8IUA4	Q8iua4 homo sapien
2	4289	72.4	1162	11	Q8BGM9	Q8bgm9 mus musculu
3	4277.5	72.2	1163	11	Q8K3G8	Q8k3g8 mus musculu
4	3658.5	61.8	1046	11	Q8BGK7	Q8bgk7 mus musculu
5	2580.5	43.6	720	11	Q7TNB7	Q7tnb7 mus musculu
6	2527	42.7	639	11	Q8K290	Q8k290 mus musculu
7	2233	37.7	578	11	Q80W95	Q80w95 mus musculu
8	1531	25.8	392	4	Q96B16	Q96b16 homo sapien
9	1201.5	20.3	375	11	Q8BHF5	Q8bhf5 mus musculu
10	1163	19.6	356	11	Q8BH78	Q8bh78 mus musculu
11	1152.5	19.5	357	11	Q8K3G7	Q8k3g7 mus musculu
12	901	15.2	184	6	Q7YRW9	Q7yrw9 bos taurus
13	887	15.0	199	13	Q7T224	Q7t224 gallus gall
14	867	14.6	179	6	Q9GM33	Q9gm33 macaca fasc
15	788.5	13.3	760	13	Q90638	Q90638 gallus gall
16	779	13.2	780	11	Q8K4S4	Q8k4s4 mus musculu
17	778	13.1	780	11	Q8K0T0	Q8k0t0 mus musculu
18	755.5	12.8	214	13	Q7T222	Q7t222 carassius a
19	699	11.8	643	11	Q8CCU2	Q8ccu2 mus musculu
20	688	11.6	199	4	Q9BQ59	Q9bq59 homo sapien
21	672	11.3	208	13	Q90637	Q90637 gallus gall
22	671	11.3	267	11	Q63765	Q63765 rattus sp.
23	626	10.6	237	11	Q8C6D5	Q8c6d5 mus musculu
24	623.5	10.5	236	11	Q8VBU0	Q8vbu0 rattus norv
25	586	9.9	221	13	Q7ZUD6	Q7zud6 brachydanio
26	566	9.6	595	5	Q9VMV9	Q9vmv9 drosophila
27	528	8.9	234	5	Q9VMW3	Q9vmw3 drosophila
28	528	8.9	2484	5	Q9U347	Q9u347 caenorhabdi
29	526	8.9	224	5	Q9VMW1	Q9vmw1 drosophila
30	520	8.8	222	5	Q9VMW4	Q9vmw4 drosophila
31	519.5	8.8	2607	5	Q23187	Q23187 caenorhabdi
32	518	8.7	202	5	Q9VMW2	Q9vmw2 drosophila
33	358.5	6.1	1417	3	Q871Y7	Q871y7 neurospora
34	357.5	6.0	2768	5	Q9VC00	Q9vc00 drosophila
35	343	5.8	107	13	Q7T223	Q7t223 carassius a
36	341.5	5.8	5412	5	Q9W596	Q9w596 drosophila
37	340.5	5.7	222	5	Q23188	Q23188 caenorhabdi
38	339	5.7	1150	5	Q8IMM6	Q8imm6 drosophila
39	334	5.6	16215	5	Q9NFS3	Q9nfs3 drosophila
40	334	5.6	18074	5	Q9I7U4	Q9i7u4 drosophila
41	331	5.6	7962	4	Q10465	Q10465 homo sapien
42	331	5.6	34350	4	Q8WZ42	Q8wz42 homo sapien
43	325.5	5.5	5327	5	O76891	O76891 drosophila
44	322.5	5.4	846	5	Q8MRP6	Q8mrp6 drosophila
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# ALIGNMENTS

## RESULT 1

Q8IUA4

ID Q8IUA4 PRELIMINARY; PRT; 986 AA.  
AC Q8IUA4;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE RNT4 (RTN4).  
 GN RTN4.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Oertle T., van der Putten H., Schwab M.E.;  
 RT "Genomic Structure and Functional Characterization of the Promoter  
 RT Structures of Human and Mouse Nogo/Rtn-4.";  
 RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Oertle T., Schwab M.E.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Van der Putten H.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RX MEDLINE=22376540; PubMed=12488097;  
 RA Oertle T., van der Putten H., Schwab M.E.;  
 RT "Genomic Structure and Functional Characterization of the Promoter  
 RT Structures of Human and Mouse Nogo/Rtn-4.";  
 RL J. Mol. Biol. 325:299-323(2003).  
 DR EMBL; AY102285; AAM64244.1; -.  
 DR EMBL; AY123245; AAM64249.1; -.  
 DR EMBL; AY123246; AAM64250.1; -.  
 DR EMBL; AY123247; AAM64251.1; -.  
 DR EMBL; AY123248; AAM64252.1; -.  
 DR EMBL; AY123249; AAM64253.1; -.  
 DR EMBL; AY123250; AAM64254.1; -.  
 DR GO; GO:0005783; C:endoplasmic reticulum; IEA.  
 DR InterPro; IPR003388; Reticulon.  
 DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS50845; RETICULON; 1.  
 SQ SEQUENCE 986 AA; 108449 MW; 0CDE8F647036415A CRC64;

Query Match 81.9%; Score 4851; DB 4; Length 986;  
 Best Local Similarity 98.9%; Pred. No. 2.4e-231;  
 Matches 976; Conservative 1; Mismatches 8; Indels 2; Gaps 2;

Qy	193	MDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAASFKEHEYLGNLSTVLPTTEGTLQ	252
Db	1	MDLKEQPGNTISAGQEDFPSVLLETAASLPSLSPLSAASFKEHEYLGNLSTVLPTTEGTLQ	60
Qy	253	ENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSVSPKAESAVIVANPREEIIIVK	312
Db	61	ENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSVSPKAESAVIVANPREEIIIVK	120
Qy	313	NKDEEEKLVSNILHXQQELPTALTCLKVKEDEVVSSEKAKDSFNEKRVAVEAPMREEYAD	372
Db	121	NKDEEEKLVSNILHNQQELPTALTCLKVKEDEVVSSEKAKDSFNEKRVAVEAPMREEYAD	180

Qy	373	FKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSSESSNDDTS	432
Db	181	FKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNHEKDSSESSNDDTS	240
Qy	433	FPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSENXTDEKKIEEKKAQIVT	492
Db	241	FPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSENXTDEKKIEEKKAQIVT	300
Qy	493	EKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTEEVVANMPEGLTPDLVQEACESELNEV	552
Db	301	EKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTEEVVANMPEGLTPDLVQEACESELNEV	360
Qy	553	TGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPDIVMEAPLNSAVPS	612
Db	361	TGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPDIVMEAPLNSAVPS	420
Qy	613	AGASVIQPSSSPLEASSVNYESIKHEPENPPPYEEAMSVSL-KVSGIKEEIKEPENINAA	671
Db	421	AGASVIQPSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKKVSGIKEEIKEPENINAA	480
Qy	672	LQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELVEDSSPDSEPVD	731
Db	481	LQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELVEDSSPDSEPVD	540
Qy	732	LFSDDSIIPDVPQKQDETVMVLVKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLS	791
Db	541	LFSDDSIIPDVPQKQDETVMVLVKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLS	600
Qy	792	LDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFIKSEAQIRETETFSDDSSPIE	851
Db	601	LDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFIKSEAQIRETETFSDDSSPIE	660
Qy	852	IIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIQP	911
Db	661	IIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIQP	720
Qy	912	KVEEKISFSDDFSKNGSATSQVLLLPDVSALGHTQAEIESIVKPKVLEKEAEKKLPSDT	971
Db	721	KVEEKISFSDDFSKNGSATSQVLLLPDVSALA-TQAEIESIVKPKVLVKEAEKKLPSDT	779
Qy	972	EKEDRSPSAIFSAIDLKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIAL	1031
Db	780	EKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIAL	839
Qy	1032	ALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKE	1091
Db	840	ALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKE	899
Qy	1092	LRRFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHY	1151
Db	900	LRRFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHY	959
Qy	1152	LGLANKNVKDAMAKIQAKIPGLKRKAE	1178
Db	960	LGLANKNVKDAMAKIQAKIPGLKRKAE	986

## Q8BGM9

Query Match 72.4%; Score 4289; DB 11; Length 1162;  
Best Local Similarity 73.9%; Pred. No. 1.7e-203;  
Matches 883; Conservative 109; Mismatches 153; Indels 50; Gaps 18;

Qy	1	MEDLDQSPVLVSSS--DSPRRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKP	59
		:                            :   :   :	
Db	1	MEDIDQSSLVSSSADSPRRPPPAFKYQFVTEPEDEEDEDEDEDEDEDLEELEVLERKP	60
Qy	60	AAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPA	119
		:   :                     :   :	
Db	61	AAGLSAAPVP--PAA-APLLDFSSDSVPPAPRGPLPAAPPPTAPERQPSWERSPAAS---A	114

Qy 120 PSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRR 179  
 || |||| ||||| || || || || ||||| |||||  
 Db 115 PSLPPAAAVLPSKLPEDDEPPAR--PPAPAGASPLAE-----PAAPPSTPAAPKRR 163

Qy 180 GSSG-----AVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLS 225  
 || : ||||| ||||| ||||| |||||  
 Db 164 GSGSVDETLFALPAASEPVI PSSAEKIMDLKEQPGNTVSSGQEDFPSVLFETAASLPSLS 223

Qy 226 PLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSE 285  
 ||| |||| ||||| | ||||:| :|||:| :| :||| |||||  
 Db 224 PLSTVSFKEHGYLGNL SAVASTEGTIEETLNEASRELPERATNPFVNRESAEFSVLEYSE 283

Qy 286 MGSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTCLKVKEDEV 345  
 |||||: ||| |||:| | :||:|:|:|:| :| :| || | |||:| ||| |  
 Db 284 MGSSFNKSPKGESAMLVENTKEEVIVRSKDKED-LVCSAALHNPQESPATLTKVVKEDGV 342

Qy 346 VSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNLES 404  
 :| || | ||| :||| ||:|||||||:| ||||:| | | :||| :|||  
 Db 343 MSPEKTMDFNEMKMSVVAPVREEYADFKPFQAWEVKDTYEGSRDLAA----RANMES 398

Qy 405 KVDKKCFADSLEQTNHEKDSSESNDDTSFSPSTPEGIKDRSGAYITCAPFNPAATESIATN 464  
 ||||| |||| | |||| |:| ||| ||| :|| | |||| |: :||| | |  
 Db 399 KVDKKCFEDSLEQKGHGKDSERNENASFPRTPELVKDGSRAYITCDSFS-SATESTAN 457

Qy 465 IFPLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKV 524  
 |||:| ||| ||||| ||||:| ||| || ||||| || || |||||:| ||  
 Db 458 IFPVLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFLVAIHDSEADYVTTDNLISKV 516

Qy 525 TEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCP 584  
 || ||| ||||| ||||| ||||| ||||| ||||| :|||:| |||||  
 Db 517 TEAVVATMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESIYPTAQLCP 576

Qy 585 SFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEA-SSVNYESIKHEPENPP 643  
 ||||:||||| ||||| :|| |||| |||:| || | |:| :| |||||  
 Db 577 SFEEAEATPSPVLPDIVMEAPLNSLLPSTGASVAQPSASPLEVSPVSYDGIKLEPENPP 636

Qy 644 PYEEAMSVSLKVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDY 703  
 |||||:| || | |||||:| || | ||||| ||||| |||:|:|:|  
 Db 637 PYEEAMSVALKTSDSKEEIKEPESFNAAAQEAEPYISIIACDLIKETKLSTEPSPEFSNY 696

Qy 704 SEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFES 763  
 ||:| | :| ||| |||:| |||:| |||||:| || | |:| |||:| |||| | |:|  
 Db 697 SEIAKFEKSVDPDHCELVDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVS-ET 755

Qy 764 MIEYENKEKLSALPPEGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTA 823  
 : :||:|:| || | |||||:| :| ||| :|:| ||:| ||| :||  
 Db 756 VTQHKHKERLSASPQEVGKPYLESFQPNLHITKDA-ASNEIPTLTKKETISLQMEEFNTA 814

Qy 824 VYSNDDLFIKSEAQIRETETFSDDSSPIEIIIDEFPTLISSKTD SFSKLAREYTDLEVSHKS 883  
 :||| ||| :||:| ||||| ||||| ||||| :||| || :||| |||:| ||  
 Db 815 IYSNDDL LSSKEDKMKESETFSDSSPIEIIIDEFPTFVSAKDDS----PKEYTDLEVSNKS 870

Qy 884 EIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNKSATSKVLLLPPDVSA 943  
 |||| || ||||:| || || || | : ||:|:| :| || || |:| ||  
 Db 871 EIANVQSGANSLPCSELPCDLSFKNTYPKDEAHV--SDEFKSRSSSVKVP LLLPNVSAL 928

Qy 944 GHTQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIF SADLGKTSVVDLLYWRDIKKT 1003



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Qy      1 MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKP 59
      |||:||||| ||||| ||||| |||||:|:|:|:|:|:|:|:|:|:|:|:|:|
Db      1 MEDIDQSSLVSSSADSPRPPPAFKYQFVTEPEDEEDEEDEEEEEDEDEDLEELEVLERKP 60

Qy     60 AAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSVSVSTVPA 119
      ||||| ||| ||| |||:| | :| ||||| ||||| |||||:| | :| | |
Db     61 AAGLSAVPVP--PAA-APLLDFSSDSVPPAPRGPLPAAPPTAPERQPSWERSPAAS--A 114

Qy    120 PSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRR 179

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Db	115	PSLPPAAAVLPSKLPEDDEPPAR--PPAPAGASPLAE-----PAAPPSTPAAPKRR	163
Qy	180	GSSG-----AVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLS	225
Db	164	GS GSVDETLFALPAASEPVI PSSAEKIMDLKEQPGNTVSSGQEDFPSVLFETAASLPSLS	223
Qy	226	PLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSE	285
Db	224	PLSTVSFKEHGYLGNLSAVASTEGTIEETLNEASRELPERATNPFVNRESAEFSVLEYSE	283
Qy	286	MGSSFSVSPKAESAVIVANPREEIIVKNKDEEEKLVSNNILHXQQELPTALTCLVKEDEV	345
Db	284	MGSSFNGSPKGESAMLVENTKEEVIVRSKDKED-LVCSAALHNPQESPATLTKVVKEDGV	342
Qy	346	VSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVVEVKDSKEDS-DMLAAGGKIESNLES	404
Db	343	MSPEKTMDFNEMKMSVVAPVREEYADFKPFEQAWEVKDTYEGSRDLAA----RANMES	398
Qy	405	KVDKKCFADSLEQTNHEKDSSESSNDTSFSPSTPEGIKDRSGAYITCAPFNPAATESIATN	464
Db	399	KVDKKCFEDSLEQKSHGKDSERENASFPSTPELVKDGSRAYITCDSFT-SATESTAN	457
Qy	465	IFPLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKV	524
Db	458	IFPVLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFLVAIHDEADYVTTDNLKSV	516
Qy	525	TEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCP	584
Db	517	TEAVVATMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESIYPTAQLCP	576
Qy	585	SFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEA-SSVNYESIKHEPENPP	643
Db	577	SFEEAEATPSPVLPDIVMEAPLNSLLPSTGASVAQPSASPLEVPSVSYDGIKLEPENPP	636
Qy	644	PYEEAMSVSLKVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDY	703
Db	637	PYEEAMSVALKTSDAKEEIKEPESFNAAAQEAEPYISIIACDLIKETKLSTEPSPGFSNY	696
Qy	704	SEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLVKESLTETSFES	763
Db	697	SEIAKFEKSVDPDHCELVDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTVES-ET	755
Qy	764	MIEYENKEKLSALPPEGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTA	823
Db	756	VTQHKHKERLSASPQEVGKPYLESFQPNLHITKDA-ASNEIPTLTKKETISLQMEEFNTA	814
Qy	824	VYSNDDLFIKSEAQIRETETFSDDSSPIEIIIDEFPTLISSKTDSSFKLAREYTDLEVSHKS	883
Db	815	IYSNDDLSSKEDKMKESETFSDSSPIEIIIDEFPTFVSAKDDS----PKEYTDLEVSNKS	870
Qy	884	EIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPDVSAL	943
Db	871	EIANVQSGANSLPCSELPCDLSFKNTYPKDEAHV--SDEFKSRSSSVKVPLLLPNVSA	928
Qy	944	GHTQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKT	1003

Db 929 -ESQIEMGNIVKPKVLTKEAEKLPDTEKEDRSLTAVLSAELNKTSVVDLLYWRDIKKT 987

Qy 1004 GVV-FGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPPFRAY 1062  
 ||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db 988 GVVYFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPPFRAY 1047

Qy 1063 LESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLVDLKFVAVLMWVFTYVVGALFN 1122  
 |||||||||||||||||||| ||||||||||||||||||||||||||||||||||||

Db 1048 LESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLVDLKFVAVLMWVFTYVVGALFN 1107

Qy 1123 GLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178  
 |||||||||||||:|||||||||||||||:|||||||||||||||

Db 1108 GLTLLILALISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAE 1163

#### RESULT 4

Q8BGK7

ID Q8BGK7 PRELIMINARY; PRT; 1046 AA.

AC Q8BGK7;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE RTN4.

GN RTN4.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=129/SvcJ7, and 129SvcJ7;

RA Oertle T., van der Putten H., Schwab M.E.;

RT "Genomic Structure and Functional Characterization of the Promoter

RT Structures of Human and Mouse Nogo/Rtn-4.";

RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=129/SvcJ7, and 129SvcJ7;

RA Oertle T., Schwab M.E.;

RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=129/SvcJ7;

RA Van der Putten H.;

RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RC STRAIN=129SvcJ7;

RA Van der Putten H., Mir A.;

RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AY102280; AAM73502.1; -.

DR EMBL; AY102286; AAM73507.1; -.

DR MGD; MGI:1915835; Rtn4.

DR GO; GO:0005783; C:endoplasmic reticulum; IDA.

DR GO; GO:0007399; P:neurogenesis; IDA.

DR InterPro; IPR003388; Reticulon.

DR Pfam; PF02453; Reticulon; 1.

DR PROSITE; PS50845; RETICULON; 1.  
SQ SEQUENCE 1046 AA; 114221 MW; 8CE2E2238ED51222 CRC64;

Query Match 61.8%; Score 3658.5; DB 11; Length 1046;  
Best Local Similarity 69.5%; Pred. No. 2e-172;  
Matches 767; Conservative 108; Mismatches 148; Indels 81; Gaps 17;

```
Qy      97 APPVAPERQ-----PSWDPS-----PVSSTVPAP---SPLSAAVSPSKLPED 136
      |||:| | :| || | || | | |||
Db      2 APPLAGGGQKGAASEAWVPSLFVGVSGSTCTAAKSLVPIPARSSRLSAA----- 51

Qy     137 DEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKRRGSSGAVVXXXXKIMDLK 196
      : | :: || |: | |: : |||||
Db      52 -----RNETLFALPA--ASEPVIPSSAE-----KIMDLK 78

Qy     197 EQPGNTISAGQEDFPSVLLETAASXPSLSPLSAA SFKEHEYLG N LSTVLPTEGTLQENV S 256
      |||||:|:||||||| ||||| ||||| ||||| ||||| | ||||:| : :
Db      79 EQPGNTVSSGQEDFPSVL FETAASLPSLSPLSTVSFKEHGYLG N LSAVASTEGTIEETLN 138

Qy     257 EASKEVSEKAKTLLIDRDLTEFSELEYSEMGS SFVS PKAESAVIVANPREEIIVKNKDE 316
      |||:|: |:| :|:| ||| ||||| |||||: ||| |||:| | :|:|:|:|:|:|
Db     139 EASRELPERATNPFVNRESAEFSVLEYSEMGS SFNGSPKGESAMLVENTKEEVIVRSKDK 198

Qy     317 EEKLVSNNILHXQQELPTALT KL VKED EVSSEKAKDSFNEKRVAVEAPMREEYADFKPF 376
      |: || : || || | |||:|||| |:| || | ||| ::| |:| ||||| |||
Db     199 ED-LVCSAALHNPQESPATLT KV VKEDGVMSPEKTMDFNEMKMSVVAPVREEYADFKPF 257

Qy     377 ERVWEVKDSKEDS-DMLAAGGKIESNLESKV DKKCFADSLEQTNHEKDSSESNDDTSFPS 435
      |: ||||: | | |:||| :|:||||||| |||| | |||| |:| |||
Db     258 EQAWEVKDTYEGSRDVLAA----RANMESKV DKKCFEDSLEQKGHGKDSERNENASFPR 313

Qy     436 TPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSENXTDEKKIEEKKAIQVTEKN 495
      ||| :|| | |||| |: :||| | |||:||| ||| |||||:| |||:| |||
Db     314 TPELVKDGSRAYITCDSFS-SATESTAANIFPVLEDHTSENKTDEKKIEERKAQIITEK- 371

Qy     496 TSTKTSNPFVVAQDSETDYVTTDNLT KVTEE VVANMPEGLTPDLVQEACESELNEVTGT 555
      || ||||| || ||| |||||:| ||| ||| ||||| ||||| ||||| |||
Db     372 TSPKTSNPFVVAIH DSEADYVTTDNLSKVTEAVVATMPEGLTPDLVQEACESELNEATGT 431

Qy     556 KIA YETKMDLVQTSEVMQESLYPAAQLCPSFE ESEATPSPVLPDIVMEAPLNSAVPSAGA 615
      |||||:| ||||| :||:| |||||:| ||||| ||||| ||||| :|| |||
Db     432 KIA YETKVDLVQTSEAIQESIYPTAQLCPSFE EAEATPSPVLPDIVMEAPLNSLLPSTGA 491

Qy     616 SVIQPSSSPLEA-SSVNYESIKHEPENPPPYEEAMSVSLKVSGIKEEIKEPENINAALQE 674
      || |||:||| | |:|: || ||||| |||||:| | |||||: ||| |||
Db     492 SVAQPSASPLEVPSPVSYDGIKLEPENPPPYEEAMSVALKTSDSKEEIKEPESFNAAAQE 551

Qy     675 TEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQPVPDHSELVEDSSPDSEPVDLFS 734
      ||||| ||||| ||||| |||:|:|:|:|:| |: ||| |||:| |||:| |||||
Db     552 AEAPYISIACDLIKETKLSSTEPSP EFSNYSEIAKFEKSVPDHC ELVDDSSPESEPVDLFS 611

Qy     735 DDSIPDV PQQDETVM LVKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLSLDN 794
      |||||:| || |:| |||:| ||| | |: : : : |:| || | |||||: |:|
Db     612 DDSIPEVPQTQEEAVMLMKESLTEVS-ETVTQHKHKERLSASPQEVGKPYLESFQPNLHI 670

Qy     795 TKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFI SKEAQIRETETFS DSSPIEIID 854
      ||| :|: ||:| || | |||| |:|:| |||| ||| : : |:| ||||| |||||
```

Db 671 TKDA-ASNEIPTLTKKETISLQMEEFNTAIYSNDDLLSSKEDKMKESETFSDSSPIEIID 729

Qy 855 EFPTLISSKTDSEFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIPKVE 914  
 |||| :|:| || :|||||:||||| || |||:| | || || |

Db 730 EFPTFVSAKDDS----PKEYTDLEVSNKSEIANVQSGANSLPCSELPCDLSFKNTYPKDE 785

Qy 915 EKISFSDDFSKNGSATSKVLLLPDVSALGHTQAEIESIVKPKVLEKEAEKKLPSDTEKE 974  
 : ||:|:| :| || || | :||| :| | : :||||| |||:|||||

Db 786 AHV--SDEFSKSRSSSVSKVPLLLPNVSAL-ESQIEMGNIVKPKVLTKEAEKKLPSDTEKE 842

Qy 975 DRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALL 1034  
 ||| :|: ||:| ||||| ||||| ||||| ||||| ||||| |||||

Db 843 DRSILTAVLSAELNKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALL 902

Qy 1035 SVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRR 1094  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 903 SVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSALGHVNSTIKELRR 962

Qy 1095 LFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGL 1154  
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 963 LFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGL 1022

Qy 1155 ANKNVKDAMAKIQAKIPGLKRKAE 1178  
 |||:||||| |||||

Db 1023 ANKSVKDAMAKIQAKIPGLKRKAE 1046

# RESULT 5

## Q7TNB7

ID Q7TNB7 PRELIMINARY; PRT; 720 AA.

AC Q7TNB7;

DT 01-OCT-2003 (TrEMBLrel. 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Hypothetical protein.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=C57BL/6; TISSUE=Brain;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,



Db	517	TEAVVATMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESIYPTAQLCP	576
QY	585	SFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQPPSSPLEA-SSVNYESIKHEPENPP	643
Db	577	SFEEAEATPSPVLPDIVMEAPLNSLLPSTGASVAQPSASPLEVPSVSYDGIKLEPENPP	636
QY	644	PYEEAMSVSLKVSIGIKKEIKPENINAAALQETEAPYISIIACDLIKETKLSAEPAPDFSDY	703
Db	637	PYEEAMSVALKTSDSKKEIKEPESFNAAQAEAPYISIIACDLIKETKLSTEPSPEFSNY	696
QY	704	SEMAKVEQVPDPHSELVEDSSPDS	727
Db	697	SEIAKFEKSVPDPHCELVDSSPES	720

Q8K290

```

ID      Q8K290          PRELIMINARY;          PRT;    639 AA.
AC      Q8K290;
DT      01-OCT-2002 (TrEMBLrel. 22, Created)
DT      01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT      01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE      Hypothetical protein.
GN      RTN4.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Strausberg R.;
RL      Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
DR      EMBL; BC032192; AAH32192.1; -.
DR      MGD; MGI:1915835; Rtn4.
DR      GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR      GO; GO:0007399; P:neurogenesis; IDA.
DR      InterPro; IPR003388; Reticulon.
DR      Pfam; PF02453; Reticulon; 1.
DR      PROSITE; PS50845; RETICULON; 1.
KW      Hypothetical protein.
SQ      SEQUENCE    639 AA;  70312 MW;  309A19DA37603F11 CRC64;

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Qy	532	MPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEA	591
Db	1	MPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESIYPTAQLCPSFEEAEA	60
Qy	592	TPSPVLPDIVMEAPLNSAVPSAGASVIQPSSSPLEA-SSVNYESIKHEPENPPPYEEAMS	650
Db	61	TPSPVLPDIVMEAPLNSLLPSTGASVAQPSASPLEVPSVSYDGIKLEPENPPPYEEAMS	120
Qy	651	VSLKVGSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFS DYSEMAKVE	710
		:	
Db	121	VALKTSDAKEEIKEPESFNAAAQEAEPYISIACDLIKETKLSTEPSPEFSNYSEIAKFE	180





FT NON\_TER 1 1  
SQ SEQUENCE 578 AA; 63696 MW; 832670C171E4AC61 CRC64;

Query Match 37.7%; Score 2233; DB 11; Length 578;  
Best Local Similarity 78.4%; Pred. No. 2.2e-102;  
Matches 460; Conservative 52; Mismatches 65; Indels 10; Gaps 6;

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Qy      593 PSPVLPDIVMEAPLNSAVPSAGASVIQSSSSPLEA-SSVNYESIKHEPENPPPYEEAMSV 651
          ||||| :|| ||| ||:|||| | |:|: || |||||
Db      1 PSPVLPDIVMEAPLNSLLPSTGASVAQPSASPLEVPSVSYDGIKLEPENPPPYEEAMSV 60

Qy      652 SLKVSGIKEEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSEMAKVEQ 711
          :|| | |||||: ||| || ||||| ||:| ||:||||:| |:
Db      61 ALKTSDAKEEIKEPESFNAAQEAEPYISIIACDLIKETKLSTEPSPGFSNYSEIAKFEK 120

Qy      712 PVPDHSELVEDSSPDSEPVDFLSDDSIPDVPQKQDETVMVLVKESLTETSFESMIEYENKE 771
          |||| |||:||||:|||||:|||| |:| |||:|||| | |:| ::::|
Db      121 SVPDHCELVDSSPESEPVDFLSDDSIPEVPQTQEEAVMLMKESLTEVS-ETVTQHKHKE 179

Qy      772 KLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLF 831
          :||| | | |||||: :| ||| :|: ||:| | |||| :||:||||
Db      180 RLSASPQEVGKPYLESFQPNLHITKDA-ASNEIPTLTKKETISLQMEEFNTAIYSNDDLL 238

Qy      832 ISKEAQIRETETFSDDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDG 891
          ||| ::|:|||||:||||| :|:| || :|||||:||||| |
Db      239 SSKEDKMKESETFSDSSPIEIIDEFPTFVSAKDDS----PKEYTDLEVS NKSEIANVQSG 294

Qy      892 AGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSNGSATSKVLLLPDVSALGHTQAEIE 951
          | |||:||| || || | | : ||:|: |: || || |:||| :| |:
Db      295 ANSLPCSELPCDLSFKNTYPKDEAHV--SDEFSKSRSSVFKVPLLLPNVSAL-ESQIEMG 351

Qy      952 SIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASL 1011
          :||||| |||:|||||:||||| :|: ||:| |||||
Db      352 NIVKPKVLTKEAEKKLPDTEKEDRSLTAVLSAELNKTSVVDLLYWRDIKKTGVVFGASL 411

Qy      1012 FLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISE 1071
          |||||
Db      412 FLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISE 471

Qy      1072 ELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILAL 1131
          |||||
Db      472 ELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILAL 531

Qy      1132 ISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
          ||||:|||||:|||||
Db      532 ISLFSIPVIYERHQAQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAE 578
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RESULT 8

Q96B16

ID Q96B16 PRELIMINARY; PRT; 392 AA.

AC Q96B16;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)

DE Hypothetical protein (RTN4).

GN RTN4.

OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Kidney;  
 RA Strausberg R.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Oertle T., van der Putten H., Schwab M.E.;  
 RT "Genomic Structure and Functional Characterization of the Promoter  
 RT Structures of Human and Mouse Nogo/Rtn-4.";  
 RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Oertle T., Schwab M.E.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Van der Putten H.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=22376540; PubMed=12488097;  
 RA Oertle T., van der Putten H., Schwab M.E.;  
 RT "Genomic Structure and Functional Characterization of the Promoter  
 RT Structures of Human and Mouse Nogo/Rtn-4.";  
 RL J. Mol. Biol. 325:299-323(2003).  
 DR EMBL; BC016165; AAH16165.1; -.  
 DR EMBL; AY102285; AAM64242.1; -.  
 DR EMBL; AY102278; AAM64247.1; -.  
 DR GO; GO:0005783; C:endoplasmic reticulum; IEA.  
 DR InterPro; IPR003388; Reticulon.  
 DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS50845; RETICULON; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 392 AA; 42274 MW; D7B2AA5E839E58AD CRC64;

Query Match 25.8%; Score 1531; DB 4; Length 392;  
 Best Local Similarity 32.4%; Pred. No. 6.1e-68;  
 Matches 382; Conservative 7; Mismatches 3; Indels 786; Gaps 4;

QY 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 1 MEDLDQSPLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA 60  
 QY 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSVTPAP 120  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 61 AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSVTPAP 120  
 QY 121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKRRG 180  
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||  
 Db 121 SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPSTPAAPKRRG 180  
 QY 181 SSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAAASFKEHEYLGN 240

	:	
Db	181 SSGSV-----	185
Qy	241 LSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSFSVSPKAESAV	300
Db	186 -----	185
Qy	301 IVANPREEIIVKNKDEEEKLVSNILHXQQELPTALTCLVKEDEVVSSEKAKDSFNEKRV	360
Db	186 -----	185
Qy	361 AVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTNH	420
Db	186 -----	185
Qy	421 EKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFLLEDPTSENXTDE	480
Db	186 ----- :	190
Qy	481 KKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTQVTEEVVANMPEGLTPDL	540
Db	191 -----	190
Qy	541 VQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPDI	600
Db	191 -----	190
Qy	601 VMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSGIKE	660
Db	191 ----- : :	195
Qy	661 EIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQPVPDHSELV	720
Db	196 -----	195
Qy	721 EDSSPDSEPVDLFSDDSIIPDVPQKQDETVMVLKESLTETSFESMIEYENKEKLSALPPEG	780
Db	196 -----	199
Qy	781 GKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFISKEAQIRE	840
Db	200 -----	199
Qy	841 TETFSDDSSPIEIIDFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTEL	900
Db	200 -----	199
Qy	901 PHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSA LGHTQAEIESIVKPKVLE	960
Db	200 -----	199
Qy	961 KEAEKKLPSDTEKEDRSPSAIF SADLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVF	1020
Db	200 -----: :	234
Qy	1021 SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS	1080

Db 235 SIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNS 294

QY 1081 ALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI 1140  
 |||

Db 295 ALGHVNCTIKELRRLFLVDDLVDSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVPVI 354

QY 1141 YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178  
 |||

Db 355 YERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 392

RESULT 9

Q8BHF5

ID Q8BHF5 PRELIMINARY; PRT; 375 AA.

AC Q8BHF5;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE RTN4.

GN RTN4.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=129/SvcJ7, and 129SvcJ7;

RA Oertle T., van der Putten H., Schwab M.E.;

RT "Genomic Structure and Functional Characterization of the Promoter

RT Structures of Human and Mouse Nogo/Rtn-4.";

RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=129/SvcJ7, and 129SvcJ7;

RA Oertle T., Schwab M.E.;

RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=129/SvcJ7;

RA Van der Putten H.;

RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

RN [4]

RP SEQUENCE FROM N.A.

RC STRAIN=129SvcJ7;

RA Van der Putten H., Mir A.;

RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AY102282; AAM73504.1; -.

DR EMBL; AY102286; AAM73509.1; -.

DR MGD; MGI:1915835; Rtn4.

DR GO; GO:0005783; C:endoplasmic reticulum; IDA.

DR GO; GO:0007399; P:neurogenesis; IDA.

DR InterPro; IPR003388; Reticulon.

DR Pfam; PF02453; Reticulon; 1.

DR PROSITE; PS50845; RETICULON; 1.

SQ SEQUENCE 375 AA; 40300 MW; 23D9EB19BE671AE6 CRC64;

Query Match 20.3%; Score 1201.5; DB 11; Length 375;

Best Local Similarity 28.6%; Pred. No. 1.1e-51;  
Matches 337; Conservative 17; Mismatches 20; Indels 805; Gaps 11;

```
QY      1 MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKP 59
      |||:| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      1 MEDIDQSSLVSSSADSPPRPPPAFKYQFVTEPEDEDEDEDEDEDEDEDEDLEELEVLERKP 60

QY     60 AAGLSAAPVPTAPAAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSTVPA 119
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db     61 AAGLSAAPVP--PAA-APLLDFSSDSVPPAPRGPLPAAPPPTAPERQPSWERSPAAS---A 114

QY    120 PSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVWTPPAPAPAAPSTPAAPKRR 179
      || | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db    115 PSLPPAAAVLPSKLPEDDEPPAR--PPAPAGASPLAE-----PAAPPSTPAAPKRR 163

QY    180 GSSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAAASFKEHEYLG 239
      ||
Db    164 GS----- 165

QY    240 NLSTVLPTTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSVSPKAESA 299
Db    166 ----- 165

QY    300 VIVANPREEIIVKNKDEEEKLVSNILHXQQELPTALTCLKVKEDEVVSSEKAKDSFNEKR 359
Db    166 ----- 165

QY    360 VAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDDKKCFADSLEQTN 419
Db    166 ----- 165

QY    420 HEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSENXTD 479
      | : | |
Db    166 -----GSVDETLF----- 173

QY    480 EKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTEEVVANMPEGLTPD 539
Db    174 ----- 173

QY    540 LVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLPD 599
Db    174 ----- 173

QY    600 IVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSGIK 659
      | : | |
Db    174 -----ALPAA----- 178

QY    660 EEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSEL 719
Db    179 ----- 178

QY    720 VEDSSPDSEPVDLFSDDSIIPDVPQKQDETVMVLKESLTETSFESMIEYENKEKLSALPPE 779
      || | |
Db    179 -----SEPV----- 182

QY    780 GGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFIKSEAQIR 839
```

Db 183 ----- 182

QY 840 ETETFSDDSSPIEIIDFPTLISSKTDSEFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTE 899

Db 183 ----- 182

QY 900 LPHDLSLKNIQPKVEEKISFSDDFSKNGSATS SKVLLLPDVSALGHTQAEIESIVKPKVL 959

Db 183 ----- 182

QY 960 EKEAEKKLPDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTV 1019  
 :|| :|||||||||||||||||||||

Db 183 -----IPS-----SAVVDLLYWRDIKKTGVVFGASLFLLLSLTV 216

QY 1020 FSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSN 1079  
 |||||||||||||||||||||||||||||||||||||||

Db 217 FSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSN 276

QY 1080 SALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVVGALFNGLTLLILALISLFSVPV 1139  
 ||||| |||||||||||||||||||||||||||||||||||:|

Db 277 SALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVVGALFNGLTLLILALISLFSIPV 336

QY 1140 IYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178  
 |||||||||||||||:|||||||||||||

Db 337 IYERHQAQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAE 375

RESULT 10

Q8BH78

ID Q8BH78 PRELIMINARY; PRT; 356 AA.

AC Q8BH78;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)

DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update).

DE RTN4.

GN RTN4.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=129/SvcJ7, and 129SvcJ7;

RA Oertle T., van der Putten H., Schwab M.E.;

RT "Genomic Structure and Functional Characterization of the Promoter

RT Structures of Human and Mouse Nogo/Rtn-4.";

RL Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=129/SvcJ7, and 129SvcJ7;

RA Oertle T., Schwab M.E.;

RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

RN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=129/SvcJ7;

RA Van der Putten H.;

RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.

RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=129SvcJ7;  
 RA Van der Putten H., Mir A.;  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY102281; AAM73503.1; -.  
 DR EMBL; AY102286; AAM73508.1; -.  
 DR MGD; MGI:1915835; Rtn4.  
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.  
 DR GO; GO:0007399; P:neurogenesis; IDA.  
 DR InterPro; IPR003388; Reticulon.  
 DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS50845; RETICULON; 1.  
 SQ SEQUENCE 356 AA; 38403 MW; 4366C03BA9630B56 CRC64;

Query Match 19.6%; Score 1163; DB 11; Length 356;  
 Best Local Similarity 27.7%; Pred. No. 8e-50;  
 Matches 326; Conservative 12; Mismatches 17; Indels 824; Gaps 8;

Qy	1	MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLKRP	59
		:                            : : : : : : : : : : : :	
Db	1	MEDIDQSSLVSSSADSPPRPPPAFKYQFVTEPEDEEDEDEEEEEDEDEDLEELEVLKRP	60
Qy	60	AAGLSAAPVPTAPAAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSTVPA	119
		: : :             :   :	
Db	61	AAGLSAAPVP--PAA-APLLDFSSDSVPPAPRGPLPAAPPTAPERQPSWERSPAAS---A	114
Qy	120	PSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEVWTPPAPAPAAPPSTPAAPKRR	179
Db	115	PSLPPAAAVLPSKLPEDDEPPAR--PPAPAGASPLAE-----PAAPPSTPAAPKRR	163
Qy	180	GSSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAAFSKEHEYLG	239
Db	164	GS-----	165
Qy	240	NLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSVSPKAESA	299
Db	166	-----	165
Qy	300	VIVANPREEIIVKNKDEEEKLVSNILHXQQELPTALTKLVKEDEVVSSEKAKDSFNEKR	359
Db	166	-----	165
Qy	360	VAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTN	419
Db	166	-----	165
Qy	420	HEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSENXTD	479
Db	166	-----	165
Qy	480	EKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTEEVVANMPEGLTPD	539
Db	166	-----	165
Qy	540	LVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLDP	599

Db 166 ----- 165

Qy 600 IVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPYEEAMSVSLKVSGIK 659

Db 166 ----- 165

Qy 660 EEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSEL 719

Db 166 ----- 165

Qy 720 VEDSSPDSEPVDLFSDDSIQDVPQKQDETVMVLVKESLTETSFESMIEYENKEKLSALPPE 779

Db 166 ----- 165

Qy 780 GGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFIKSEAQIR 839

Db 166 ----- 165

Qy 840 ETETFSDDSSPIEIIIDEFPTLISSKTDSFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTE 899

Db 166 -----GSV----- 168

Qy 900 LPHDLSLKNIQPKVEEKISFSDDFSKNGSATSQVLLLPDVSALGHTQAEIESIVKPKVL 959

Db 169 ----- 168

Qy 960 EKEAEKKLPDTEKEDRSPSAIFSDLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTV 1019

Db 169 -----VVDLLYWRDIKKTGVVFGASLFLLLSLTV 197

Qy 1020 FSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSN 1079

Db 198 FSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSN 257

Qy 1080 SALGHVNCTIKELRRLFLVDDLVDSLKFVFLMWVFTYVGALFNGLTLLILALISLFSVPV 1139

Db 258 SALGHVNSTIKELRRLFLVDDLVDSLKFVFLMWVFTYVGALFNGLTLLILALISLFSIPV 317

Qy 1140 IYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178

Db 318 IYERHQAQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAE 356

RESULT 11

Q8K3G7

ID Q8K3G7 PRELIMINARY; PRT; 357 AA.

AC Q8K3G7;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)

DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Nogo-B.

GN RTN4.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]



RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/c;  
 RA Jin W., Li R., Long M., Shen J., Ju G.;  
 RT "Cloning and expression of the mouse Nogo-B protein.";  
 RL Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.  
 DR EMBL; AY114153; AAM77069.1; -.  
 DR MGD; MGI:1915835; Rtn4.  
 DR GO; GO:0005783; C:endoplasmic reticulum; IDA.  
 DR GO; GO:0007399; P:neurogenesis; IDA.  
 DR InterPro; IPR003388; Reticulon.  
 DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS50845; RETICULON; 1.  
 SQ SEQUENCE 357 AA; 38566 MW; 73BB3D17DFDBDF15 CRC64;

Query Match 19.5%; Score 1152.5; DB 11; Length 357;  
 Best Local Similarity 27.6%; Pred. No. 2.6e-49;  
 Matches 326; Conservative 12; Mismatches 17; Indels 825; Gaps 9;

Qy	1	MEDLDQSPLVSSS-DSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKP	59
		:                             : :    :	
Db	1	MEDIDQSSLVSSSADSPRRPPPAFKYQFVTEPEDEEDEDEDEDEDEDLEELEVLERKP	60
Qy	60	AAGLSAAPVPTAPAAGAPLMDFGNDVFPAPRGPLPAAPPVAPERQPSWDPSVVSSTVPA	119
		: :             :   :	
Db	61	AAGLSAAPVP--PAA-APLLDFSSDSVPPAPRGPLPAAPTAPERQPSWERSPAAS---A	114
Qy	120	PSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRR	179
Db	115	PSLPPAAAVLPSKLPEDDEPPAR--PPAPAGASPLAE-----PAAPPSTPAAPKRR	163
Qy	180	GSSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAAAFKEHEYL	239
Db	164	GS-----	165
Qy	240	NLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSVSPKAESA	299
Db	166	-----	165
Qy	300	VIVANPREEIIIVKNKDEEEKLVSNILHXQQELPTALTCLVKEDEVVSSEKAKDSFNEKR	359
Db	166	-----	165
Qy	360	VAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVDKKCFADSLEQTN	419
Db	166	-----	165
Qy	420	HEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFPLLEDPTSENXTD	479
Db	166	-----	165
Qy	480	EKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTQVTEEVVANMPEGLTPD	539
Db	166	-----	165
Qy	540	LVQEACESELNEVTGKIAETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLDP	599
Db	166	-----	165

Qy 600 IVMEAPLNSAVPSAGASVIQPSSSPLEASSVNYESIKHEPENPPPPYEEAMSVSLKVSGIK 659  
 Db 166 ----- 165  
 Qy 660 EEIKEPENINAALQETEAPYISIIACDLIKETKLSAEPAPDFSDYSEMAKVEQVPDPHSEL 719  
 Db 166 ----- 165  
 Qy 720 VEDSSPDSEPVDFLSDSIPDVPQKQDETVMVLVKESLTETSFESMIEYENKEKLSALPPE 779  
 Db 166 ----- 165  
 Qy 780 GGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFIKSEAQIR 839  
 Db 166 ----- 165  
 Qy 840 ETETFSDDSSPIEIIDEFPTLISSKTDSEFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTE 899  
 Db 166 -----GSV----- 168  
 Qy 900 LPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPPDVSAHGHTQAEIESIVKPKVL 959  
 Db 169 ----- 168  
 Qy 960 EKEAEKKLPDTEKEDRSPSAIFSDLGKTSVVDLLYWRDIKKTGVV-FGASLFLLLSLT 1018  
 Db 169 -----VVDLLYWRDIKKTGVVYFGASLFLLLSLT 197  
 Qy 1019 VFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYS 1078  
 Db 198 VFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYS 257  
 Qy 1079 NSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSVP 1138  
 Db 258 NSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILALISLFSIP 317  
 Qy 1139 VIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178  
 Db 318 VIYERHQAQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAE 357

RESULT 12

Q7YRW9

ID Q7YRW9 PRELIMINARY; PRT; 184 AA.

AC Q7YRW9;

DT 01-OCT-2003 (TrEMBLrel. 25, Created)

DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE RTN4w (Fragment).

GN RTN4.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;

OC Bovidae; Bovinae; Bos.

OX NCBI\_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A.  
RX MEDLINE=22715887; PubMed=12832288;  
RA Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;  
RT "A reticular rhapsody: phylogenic evolution and nomenclature of the  
RT RTN/Nogo gene family.";  
RL FASEB J. 17:1238-1247(2003).  
DR EMBL; AY164744; AAP47319.1; -.  
FT NON TER 1 1  
SQ SEQUENCE 184 AA; 20671 MW; DE990E03BBAF84A1 CRC64;

Query Match 15.2%; Score 901; DB 6; Length 184;  
Best Local Similarity 98.9%; Pred. No. 2.8e-37;  
Matches 182; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 995 LYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSD 1054  
|||||  
Db 1 LYWRDIKKTGVVFGXXLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSD 60  
Qy 1055 EGHPPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVF 1114  
|||||  
Db 61 EGHPPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVF 120  
Qy 1115 TYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLK 1174  
|||||  
Db 121 TYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLK 180  
Qy 1175 RKA 1178  
||||  
Db 181 RKA 184

# RESULT 13

Q7T224

ID Q7T224 PRELIMINARY; PRT; 199 AA.  
AC Q7T224;  
DT 01-OCT-2003 (TrEMBLrel. 25, Created)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE RTN4-C.  
GN RTN4.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22715887; PubMed=12832288;  
RA Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;  
RT "A reticular rhapsody: phylogenic evolution and nomenclature of the  
RT RTN/Nogo gene family.";  
RL FASEB J. 17:1238-1247(2003).  
DR EMBL; AY164737; AAP47312.1; -.  
SQ SEQUENCE 199 AA; 22293 MW; 07CF4E4EF2723251 CRC64;

Query Match 15.0%; Score 887; DB 13; Length 199;  
Best Local Similarity 88.2%; Pred. No. 1.6e-36;

Matches 180; Conservative 7; Mismatches 11; Indels 6; Gaps 1;

```
Qy      975 DRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALL 1034
      |  ||      |  |||
Db      2  DSQPSG-----WKDKVVDLLYWRDIKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALL 55

Qy     1035 SVTISFRIYKGVIAIQKSDEGHPPFRAYLESEVAISEELVQKYSNSALGHVNCTIKELRR 1094
      |||
Db      56 SVTISFRIYKGVIAIQKSDEGHPPFRAYLES DVAVSEDLIQKYSSVVLGHINGTVKELRR 115

Qy     1095 LFLVDDLVDLTKFAVLMWVFTYVGALENGLTLLILALISLFSVPVIYERHQAQIDHYLGL 1154
      |||
Db     116 LFLVDDLVDLTKFAVLMWVFTYVGALENGLTLLILALISLFSVPVIYERHQAQIDHYLGL 175

Qy     1155 ANKNVKDAMAKIQAKIPGLKRKAE 1178
      |||
Db     176 VNKNVKDAMAKIQAKIPGLKRKTE 199
```

RESULT 14

Q9GM33

ID Q9GM33 PRELIMINARY; PRT; 179 AA.  
AC Q9GM33;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Hypothetical protein.  
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;  
OC Cercopithecinae; Macaca.  
OX NCBI\_TaxID=9541;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain;  
RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,  
RA Suzuki Y., Sugano S., Hashimoto K.;  
RT "Isolation of full-length cDNA clones from macaque brain cDNA  
RT libraries.";  
RL Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.  
DR EMBL; AB049853; BAB16739.1; -.  
DR GO; GO:0005783; C:endoplasmic reticulum; IEA.  
DR InterPro; IPR003388; Reticulon.  
DR Pfam; PF02453; Reticulon; 1.  
DR PROSITE; PS50845; RETICULON; 1.  
KW Hypothetical protein.  
SQ SEQUENCE 179 AA; 19949 MW; 5F8CD4383FEE9E02 CRC64;

Query Match 14.6%; Score 867; DB 6; Length 179;

Best Local Similarity 98.3%; Pred. No. 1.3e-35;

Matches 176; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

```
Qy     1000 IKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPP 1059
      :|||
Db      1  MKKTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYRGVIAIQKSDEGHPP 60

Qy     1060 RAYLESEVAISEELVQKYSNSALGHVNCTIKELRRRLFLVDDLVDLTKFAVLMWVFTYVGA 1119
```

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Db          ||||||||||||||||||||||||||||||||||||||||:||||||||||
61 RAYLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLREAVLMWVFTYVGA 120

Qy          1120 LFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178
          ||||||||||||||||||||||||||||||||||||||||
Db          121 LFNGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 179

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RESULT 15

Q90638

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ID   Q90638          PRELIMINARY;          PRT;   760 AA.
AC   Q90638;
DT   01-NOV-1996 (TrEMBLrel. 01, Created)
DT   01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   ChS-Rex-b (RTN1-A).
GN   RTN1.
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=96386034; PubMed=8793864;
RA   Baka I.D., Ninkina N.N., Pinon L.G., Adu J., Davies A.M.,
RA   Georgiev G.P., Buchman V.L.;
RT   "Intracellular compartmentalization of two differentially spliced s-
RT   rex/NSP mRNAs in neurons.";
RL   Mol. Cell. Neurosci. 7:289-303(1996).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RX   MEDLINE=97183663;
RA   Ninkina N.N., Baka I.D., Buchman V.L.;
RT   "Rat and chicken s-rex/NSP mRNA: nucleotide sequence of main
RT   transcripts and expression of splice variants in rat tissues.";
RL   Gene 184:205-210(1997).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22715887; PubMed=12832288;
RA   Oertle T., Klinger M., Stuermer C.A., Schwab M.E.;
RT   "A reticular rhapsody: phylogenic evolution and nomenclature of the
RT   RTN/Nogo gene family.";
RL   FASEB J. 17:1238-1247(2003).
DR   EMBL; U17606; AAC60075.1; -.
DR   EMBL; AY164724; AAP47301.1; -.
DR   GO; GO:0005783; C:endoplasmic reticulum; IEA.
DR   InterPro; IPR003388; Reticulon.
DR   Pfam; PF02453; Reticulon; 1.
DR   PROSITE; PS50845; RETICULON; 1.
SQ   SEQUENCE   760 AA;  82502 MW;  465C1B429F799D5C CRC64;

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Query Match          13.3%;  Score 788.5;  DB 13;  Length 760;
Best Local Similarity 27.7%;  Pred. No. 7e-31;
Matches 296;  Conservative 115;  Mismatches 315;  Indels 341;  Gaps 38;

```

QY 143 PPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRGSSGAVVXXXXKIMDLKEQPGNT 202  
 || | : | | | | | | : |  
 Db 4 PPDPQDLLLAGTAER-W-----AAAGADEYAAGAALRDGDGA-----QQREQ 45

QY 203 ISAGQEDFPSVLLETAASXPSLSPLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEV 262  
 : | | : | | | | : : | : | : : |  
 Db 46 AFGSAREHPPVAMATA-----SPGVTASSRLFDY-----GSSSANGADSSSFYT 88

QY 263 SEKAKTLLID-----RDLTEFSELEYSEMSSFSVSPKAESAVIVANPREEIIVKNKDE 316  
 | : | | | : : | : | : : | : : |  
 Db 89 S-----LISDVHYTTPRDNTYFTGV-YQQENSPIPCSTEGFNALGHPVQDV---TGFE 139

QY 317 EEKLVSNILHXQQELPTALTKLVKEDEVVSSEKAKDSFNEKRVAVEAPMREEYADFKPF 376  
 | | | : | | : : | : | : : | : | :  
 Db 140 SRGLFS-----LDSGIEMTPAESA-----EVDKSLTDPMKVEGYKYMDI 178

QY 377 ERVWEVKDSKEDSDMLAAGGKIESNLESKVDDKKCFADSLEQTNHEKDSSESNDD--TSFP 434  
 | : | | : | | : | : | : | : | :  
 Db 179 SRPEEIK-----YQEKHDPDSEDESPDLIDEYR 206

QY 435 STPEGIKDRSGAYITCAPFNPAATESIATNIFLLEDPTSENXTDEKKIEEKAQIVTEK 494  
 || | | | : : | : | : | : : | : : | : |  
 Db 207 GTPIG----SGH--AAEPQRTTASEAIKA--PKEQDPLE---DKSFRDQHNASVVTAP 253

QY 495 NTSTKTSNPFFVAAQDSETDYVTTDNLTKVTEEVVANM---PE-----GLTP 538  
 | | | | : | : | : | : | : | : |  
 Db 254 VKITLTETPGAREATSKEASVTQPKSGLKPSHEVVPTVMVSEPEDDSPGSVTPPSSGTEP 313

QY 539 DLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLP 598  
 : : | : | | | : | : | : | : | : | : |  
 Db 314 SGSESQGGKSLSEDELISAIKEAKGFSFETSEVQQS---PAV---SAEKQEQMKMPGRP 366

QY 599 DIVMEAPLNSAVPSA--GASVIQ-PSSSPLEASSV---NYESIKHEPENPPPYEEAMSVS 652  
 : : | : : | | | : | | | | : | : | : | : |  
 Db 367 --AVPSPLDNEASSAESGDSEIELVSEDPLAAEEVLHSNYMTFSH-IGGPPP--SPASPS 421

QY 653 LKVSGIKEEIKEPENINAALQETEAPYISIACDLIKETKLSAEPAPDFS DYSEMAKVEQP 712  
 : : | : : | : | : | : | : | : | : | : | : |  
 Db 422 IQYSILREERE-----AELDSELIIESCD---ASSASEESP-----KREQD 459

QY 713 VPDHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETSFESMIEYENKEK 772  
 | : | | : : | : | : | : | : | : | : |  
 Db 460 SPLMKPMVMD-----IIE-----ENSSR 478

QY 773 LSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFI 832  
 || |  
 Db 479 ASADYE----- 485

QY 833 SKEAQIRETETFS DSSPIEIIDEFPTLISSKTD SFSKLAREYTDLEVSHKSEIANAPDGA 892  
 : | | | : : | : | : | : | : | : | : |  
 Db 486 -----ASKTTE-SRMNRE-----NLADSA 503

QY 893 GSLPCTELPHDLSLKNIQPKVEEKISFSDDFS KNGSATS KVVLLPPDV SALGHTQAEIES 952  
 | : : | : | : | : | : | : | : | : | : |  
 Db 504 SYLKSS-----FVAPKVSSE-----PPTSAVSTEELKERI 533

Qy	953	IVKPKVLEKEAEKKLPDTEKEDRSPSAI-FSADLGKTSVVDLLYWRDIKKTGMVVFASL	1011
Db	534	ILKKPIEETVVNQSKVSSKDSGKRSPLALPLLPLNKQKAINLLYWRDIKQTGIVFGSLL	593
Qy	1012	FLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDGHPFRAYLESEVAISE	1071
Db	594	LLFSLTQFSVSVVAYLALAGLSATISFRIYKSVLQAVQKTDEGHPFKAYLDMEMNLSQ	653
Qy	1072	ELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILAL	1131
Db	654	DQIQKYTDCLQLYVNSTVKELRRLFLVQDLVDLSLKFAVLMWLLTYVGALFNGLTLLIMAV	713
Qy	1132	ISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1178
Db	714	VSMFTLPVVYDKYQAQIDQYGLVTRTHINTVVAQIQAKIPGAKRKAE	760

Search completed: September 29, 2004, 18:19:47  
Job time : 99.6748 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: September 29, 2004, 18:04:48 ; Search time 16.8874 Seconds  
(without alignments)  
3632.211 Million cell updates/sec

Title: US-09-830-972-29  
Perfect score: 5923  
Sequence: 1 MEDLDQSPLVSSSDSPRPQ.....VKDAMAKIQAKIPGLKRKAE 1178

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_42:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	% Query		Match Length	DB	ID	Description
	Score	Match				
1	5815	98.2	1192	1	RTN4_HUMAN	Q9nqc3 homo sapien
2	4296.5	72.5	1163	1	RTN4_RAT	Q9jkl1 rattus norv
3	915	15.4	199	1	RTN4_MOUSE	Q99p72 mus musculu
4	791	13.4	777	1	RTN1_RAT	Q64548 rattus norv
5	787.5	13.3	776	1	RTN1_HUMAN	Q16799 homo sapien
6	626	10.6	237	1	RTN3_MOUSE	Q9es97 mus musculu
7	625.5	10.6	236	1	RTN3_HUMAN	O95197 homo sapien
8	514	8.7	545	1	RTN2_HUMAN	O75298 homo sapien
9	500	8.4	471	1	RTN2_MOUSE	O70622 mus musculu
10	324.5	5.5	865	1	CPN_DROME	Q02910 drosophila
11	320	5.4	5147	1	PCLO_HUMAN	Q9y6v0 homo sapien
12	315	5.3	5038	1	PCLO_MOUSE	Q9qyx7 mus musculu
13	299	5.0	3924	1	ANK2_HUMAN	Q01484 homo sapien
14	296.5	5.0	2468	1	MAPB_HUMAN	P46821 homo sapien
15	289	4.9	2459	1	MAPB_RAT	P15205 rattus norv
16	289	4.9	2464	1	MAPB_MOUSE	P14873 mus musculu
17	287	4.8	5120	1	PCLO_CHICK	Q9pu36 gallus gall



18	286.5	4.8	3644	1	MINT_MOUSE	Q62504	mus musculu
19	276	4.7	5085	1	PCLO_RAT	Q9jks6	rattus norv
20	273.5	4.6	3664	1	MINT_HUMAN	Q96t58	homo sapien
21	264.5	4.5	8545	1	ANCL1_CAEEL	Q9n4m4	caenorhabdi
22	263.5	4.4	3396	1	PGCV_HUMAN	P13611	homo sapien
23	262.5	4.4	6632	1	UN89_CAEEL	O01761	caenorhabdi
24	260.5	4.4	3381	1	PGCV_BOVIN	P81282	bos taurus
25	259.5	4.4	1828	1	MAP2_MOUSE	P20357	mus musculu
26	258.5	4.4	2805	1	MAPA_HUMAN	P78559	homo sapien
27	258	4.4	1616	1	P200_MYCGE	Q49429	mycoplasma
28	257.5	4.3	1781	1	AK12_HUMAN	Q02952	homo sapien
29	257.5	4.3	2738	1	PGCV_RAT	Q9erb4	rattus norv
30	253	4.3	1189	1	YJH6_YEAST	P47035	saccharomyc
31	252	4.3	4377	1	ANK3_HUMAN	Q12955	homo sapien
32	250.5	4.2	1861	1	MAP2_RAT	P15146	rattus norv
33	249.5	4.2	1827	1	MAP2_HUMAN	P11137	homo sapien
34	248	4.2	3421	1	TEGU_HSVEB	P28955	equine herp
35	244	4.1	1362	1	BRD4_HUMAN	O60885	homo sapien
36	242	4.1	1790	1	USO1_YEAST	P25386	saccharomyc
37	239	4.0	1744	1	TANA_XENLA	Q01550	xenopus lae
38	238.5	4.0	1411	1	TCOF_HUMAN	Q13428	homo sapien
39	236.5	4.0	3358	1	PGCV_MOUSE	Q62059	mus musculu
40	235.5	4.0	1723	1	AIM1_HUMAN	Q9y4k1	homo sapien
41	233.5	3.9	1087	1	NFH_MOUSE	P19246	mus musculu
42	232	3.9	1140	1	YM96_YEAST	Q04893	saccharomyc
43	231	3.9	3256	1	KI67_HUMAN	P46013	homo sapien
44	229.5	3.9	1367	1	AMYH_YEAST	P08640	saccharomyc
45	228.5	3.9	1306	1	MSB2_YEAST	P32334	saccharomyc

# ALIGNMENTS

## RESULT 1

### RTN4\_HUMAN

ID RTN4\_HUMAN STANDARD; PRT; 1192 AA.  
AC Q9NQC3; O94962; Q9BXG5; Q9H212; Q9H3I3; Q9UQ42; Q9Y293; Q9Y2Y7;  
AC Q9Y5U6;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)  
DE (Neuroendocrine-specific protein) (NSP) (Neuroendocrine specific  
DE protein C homolog) (RTN-x) (Reticulon 5) (My043 protein).  
GN RTN4 OR NOGO OR ASY OR KIAA0886.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
RX MEDLINE=20129242; PubMed=10667780;  
RA Prinjha R., Moore S.E., Vinson M., Blake S., Morrow R., Christie G.,  
RA Michalovich D., Simmons D.L., Walsh F.S.;  
RT "Inhibitor of neurite outgrowth in humans."  
RL Nature 403:383-384(2000).  
RN [2]

RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RC TISSUE=Brain;  
 RX MEDLINE=21010696; PubMed=11126360;  
 RA Tagami S., Eguchi Y., Kinoshita M., Takeda M., Tsujimoto Y.;  
 RT "A novel protein, RTN-XS, interacts with both Bcl-XL and Bcl-2 on  
 RT endoplasmic reticulum and reduces their anti-apoptotic activity.";  
 RL Oncogene 19:5736-5746(2000).  
 RN [3]

RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
 RX MEDLINE=20237542; PubMed=10773680;  
 RA Yang J., Yu L., Bi A.D., Zhao S.-Y.;  
 RT "Assignment of the human reticulon 4 gene (RTN4) to chromosome  
 RT 2p14-->2p13 by radiation hybrid mapping.";  
 RL Cytogenet. Cell Genet. 88:101-102(2000).  
 RN [4]

RP SEQUENCE FROM N.A. (ISOFORM 4).  
 RA Jin W.-L., Ju G.;  
 RT "Developmentally-regulated alternative splicing in a novel Nogo-A.";  
 RL Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.  
 RN [5]

RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).  
 RC TISSUE=Placenta, and Skeletal muscle;  
 RA Ito T., Schwartz S.M.;  
 RT "Cloning of a member of the reticulon gene family in human.";  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.  
 RN [6]

RP SEQUENCE FROM N.A. (ISOFORM 2).  
 RC TISSUE=Fibroblast;  
 RA Yutsudo M.;  
 RT "Isolation of a cell death-inducing gene.";  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.  
 RN [7]

RP SEQUENCE FROM N.A. (ISOFORM 3).  
 RC TISSUE=Pituitary;  
 RA Song H., Peng Y., Zhou J., Huang Q., Dai M., Mao Y.M., Yu Y., Xu X.,  
 RA Luo B., Hu R., Chen J.;  
 RT "Human neuroendocrine-specific protein C (NSP) homolog gene.";  
 RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.  
 RN [8]

RP SEQUENCE FROM N.A. (ISOFORM 3).  
 RA Gu J.R., Wan D.F., Zhao X.T., Zhou X.M., Jiang H.Q., Zhang P.P.,  
 RA Qin W.X., Huang Y., Qiu X.K., Qian L.F., He L.P., Li H.N., Yu Y.,  
 RA Yu J., Han L.H.;  
 RT "Novel human cDNA clone with function of inhibiting cancer cell  
 RT growth.";  
 RL Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.  
 RN [9]

RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Brain;  
 RX MEDLINE=99156230; PubMed=10048485;  
 RA Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirose M.,  
 RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes. XII.  
 RT The complete sequences of 100 new cDNA clones from brain which code  
 RT for large proteins in vitro.";  
 RL DNA Res. 5:355-364(1998).  
 RN [10]

RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).  
 RC TISSUE=Brain, Ovary, Pancreas, Placenta, and Skeletal muscle;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [11]  
 RP SEQUENCE FROM N.A. (ISOFORM 3).  
 RX MEDLINE=20499367; PubMed=11042152;  
 RA Zhang Q.-H., Ye M., Wu X.-Y., Ren S.-X., Zhao M., Zhao C.-J., Fu G.,  
 RA Shen Y., Fan H.-Y., Lu G., Zhong M., Xu X.-R., Han Z.-G., Zhang J.-W.,  
 RA Tao J., Huang Q.-H., Zhou J., Hu G.-X., Gu J., Chen S.-J., Chen Z.;  
 RT "Cloning and functional analysis of cDNAs with open reading frames for  
 RT 300 previously undefined genes expressed in CD34+ hematopoietic  
 RT stem/progenitor cells.";  
 RL Genome Res. 10:1546-1560(2000).  
 RN [12]  
 RP SEQUENCE OF 482-1192 FROM N.A. (ISOFORM 1/4).  
 RC TISSUE=Brain;  
 RA Mao Y.M., Xie Y., Zheng Z.H.;  
 RL Submitted (MAY-1998) to the EMBL/GenBank/DDBJ databases.  
 RN [13]  
 RP SEQUENCE OF 186-1192 FROM N.A. (ISOFORM 1).  
 RC TISSUE=Testis;  
 RA Sha J.H., Zhou Z.M., Li J.M.;  
 RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.  
 RN [14]  
 RP TOPOLOGY.  
 RC TISSUE=Brain;  
 RX MEDLINE=20129259; PubMed=10667797;  
 RA GrandPre T., Nakamura F., Vartanian T., Strittmatter S.M.;  
 RT "Identification of the Nogo inhibitor of axon regeneration as a  
 RT Reticulon protein.";  
 RL Nature 403:439-444(2000).  
 RN [15]  
 RP FUNCTION.  
 RC TISSUE=Brain;  
 RX MEDLINE=21069055; PubMed=11201742;  
 RA Fournier A.E., Grandpre T., Strittmatter S.M.;  
 RT "Identification of a receptor mediating Nogo-66 inhibition of axonal

RT regeneration.";  
 RL Nature 409:341-346(2001).  
 RN [16]  
 RP REVIEW.  
 RX MEDLINE=21888956; PubMed=11891768;  
 RA Ng C.E.L., Tang B.L.;  
 RT "Nogos and the Nogo-66 receptor: factors inhibiting CNS neuron  
 RT regeneration.";  
 RL J. Neurosci. Res. 67:559-565(2002).  
 CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help  
 CC block the regeneration of the nervous central system in adults.  
 CC Isoform 2 reduces the anti-apoptotic activity of Bcl-xl and Bcl-2.  
 CC This is likely consecutive to their change in subcellular  
 CC location, from the mitochondria to the endoplasmic reticulum,  
 CC after binding and sequestration.  
 CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2.  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic  
 CC reticulum. Anchored to the membrane of the endoplasmic reticulum  
 CC through 2 putative transmembrane domains.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=4;  
 CC Name=1; Synonyms=RTN 4A, Nogo-A, RTN-xL;  
 CC IsoId=Q9NQC3-1; Sequence=Displayed;  
 CC Name=2; Synonyms=RTN 4B, Nogo-B, RTN-xS, Foocen-M;  
 CC IsoId=Q9NQC3-2; Sequence=VSP\_005655;  
 CC Name=3; Synonyms=RTN 4C, Nogo-C, Foocen-S;  
 CC IsoId=Q9NQC3-3; Sequence=VSP\_005652, VSP\_005653;  
 CC Name=4;  
 CC IsoId=Q9NQC3-4; Sequence=VSP\_005654;  
 CC -!- TISSUE SPECIFICITY: Isoform 1 is specifically expressed in brain  
 CC and testis and weakly in heart and skeletal muscle. Isoform 2 is  
 CC widely expressed excepted for the liver. Isoform 3 is expressed in  
 CC brain, skeletal muscle and adipocytes. Isoform 4 is testis-  
 CC specific.  
 CC -!- SIMILARITY: Contains 1 reticulon domain.  
 CC -!- CAUTION: Ref.11 sequence differs from that shown due to  
 CC frameshifts in positions 1149 and 1156.  
 CC -----  
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 CC -----  
 DR EMBL; AJ251383; CAB99248.1; -.  
 DR EMBL; AJ251384; CAB99249.1; -.  
 DR EMBL; AJ251385; CAB99250.1; -.  
 DR EMBL; AB040462; BAB18927.1; -.  
 DR EMBL; AB040463; BAB18928.1; -.  
 DR EMBL; AF148537; AAG12176.1; -.  
 DR EMBL; AF148538; AAG12177.1; -.  
 DR EMBL; AF087901; AAG12205.1; -.  
 DR EMBL; AF320999; AAG40878.1; -.  
 DR EMBL; AF132047; AAD31021.1; -.  
 DR EMBL; AF132048; AAD31022.1; -.

DR EMBL; AB015639; BAA83712.1; -.  
 DR EMBL; AF077050; AAD27783.1; -.  
 DR EMBL; AF177332; AAG17976.1; -.  
 DR EMBL; AB020693; BAA74909.1; -.  
 DR EMBL; BC001035; AAH01035.1; -.  
 DR EMBL; BC007109; AAH07109.1; -.  
 DR EMBL; BC014366; AAH14366.1; -.

Query Match 98.2%; Score 5815; DB 1; Length 1192;  
 Best Local Similarity 97.2%; Pred. No. 1.8e-215;  
 Matches 1160; Conservative 4; Mismatches 13; Indels 16; Gaps 3;

Qy	1	MEDLDQSPVLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Db	1	MEDLDQSPVLVSSSDSPPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPA	60
Qy	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP	120
Db	61	AGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDPSPVSSTVPAP	120
Qy	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Db	121	SPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRG	180
Qy	181	SSGA-----VVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSP	226
		: : :	
Db	181	SSGSVDETLFALPAASEPVIRSSAENMDLKEQPGNTISAGQEDFPSVLLETAASLPSLSP	240
Qy	227	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	286
Db	241	LSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEM	300
Qy	287	GSSFVSVPKAESAVIVANPREEIIIVKNKDEEEKLVSNILHXQQELPTALTCLKVKEDEVV	346
Db	301	GSSFVSVPKAESAVIVANPREEIIIVKNKDEEEKLVSNILHNQQELPTALTCLKVKEDEVV	360
Qy	347	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	406
Db	361	SSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKV	420
Qy	407	DKKCFADSLEQTNHEKDSSESSNDDTSFSPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	466
Db	421	DKKCFADSLEQTNHEKDSSESSNDDTSFSPSTPEGIKDRSGAYITCAPFNPAATESIATNIF	480
Qy	467	PLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFFVAAQDSETDYVTTDNLTKVTE	526
Db	481	PLLDPTSENKTDEKKIEEKKAQIVTEKNTSTKTSNPFLVAAQDSETDYVTTDNLTKVTE	540
Qy	527	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	586
Db	541	EVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSF	600
Qy	587	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	646
Db	601	EESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHEPENPPPYE	660
Qy	647	EAMSVSL-KVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSE	705

Db	661	EAMSVSLKKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEPAPDFSDYSE	720
Qy	706	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETSFESMI	765
Db	721	MAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSI PDVPQKQDETVM LVKESLTETSFESMI	780
Qy	766	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	825
Db	781	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVY	840
Qy	826	SNDDLFI SKEAQIRETETFS DSSPIEIIDEFPTLISSKTD SFSKLAREYTDLEVSHKSEI	885
Db	841	SNDDLFI SKEAQIRETETFS DSSPIEIIDEFPTLISSKTD SFSKLAREYTDLEVSHKSEI	900
Qy	886	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATS KVVLLPPDV SALGH	945
Db	901	ANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATS KVVLLPPDV SALA-	959
Qy	946	TQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIF SADLGKTSVVDLLYWRDIKKTGV	1005
Db	960	TQAEIESIVKPKVLVKEAEKKLPDTEKEDRSPSAIFSAELSKTSVVDLLYWRDIKKTGV	1019
Qy	1006	VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES	1065
Db	1020	VFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLES	1079
Qy	1066	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT	1125
Db	1080	EVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLT	1139
Qy	1126	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1178
Db	1140	LLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1192

# RESULT 2

## RTN4\_RAT

ID RTN4\_RAT STANDARD; PRT; 1163 AA.

AC Q9JK11; Q9JK10; Q9R0D9; Q9WUE9; Q9WUF0;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein) (Foocen)

DE (Glut4 vesicle 20 kDa protein).

GN RTN4 OR NOGO.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;

RN [1]

RP SEQUENCE FROM N.A. (ISOFORM 3), AND PARTIAL SEQUENCE.

RC STRAIN=Sprague-Dawley; TISSUE=Adipocyte;

RX MEDLINE=99249816; PubMed=10231557;

RA Morris N.J., Ross S.A., Neveu J.M., Lane W.S., Lienhard G.E.;

RT "Cloning and characterization of a 22 kDa protein from rat adipocytes:

RT a new member of the reticulon family.";

RL Biochim. Biophys. Acta 1450:68-76(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
 RX MEDLINE=20129258; PubMed=10667796;  
 RA Chen M.S., Huber A.B., Van der Haar M.E., Frank M., Schnell L.,  
 RA Spillmann A.A., Christ F., Schwab M.E.;  
 RT "Nogo-A is a myelin-associated neurite outgrowth inhibitor and an  
 RT antigen for monoclonal antibody IN-1.";  
 RL Nature 403:434-439(2000).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 4).  
 RC STRAIN=Wistar Kyoto; TISSUE=Vascular smooth muscle;  
 RA Ito T., Schwartz S.M.;  
 RT "Cloning of a member of the reticulon gene family in rat: one of two  
 RT minor splice variants.";  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.  
 RN [4]  
 RP FUNCTION.  
 RX MEDLINE=22033691; PubMed=12037567;  
 RA GrandPre T., Li S., Strittmatter S.M.;  
 RT "Nogo-66 receptor antagonist peptide promotes axonal regeneration.";  
 RL Nature 417:547-551(2002).  
 CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help  
 CC block the regeneration of the nervous central system in adults (By  
 CC similarity).  
 CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-xl and Bcl-2 (By  
 CC similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the  
 CC membrane of the endoplasmic reticulum through 2 putative  
 CC transmembrane domains (By similarity).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=4;  
 CC Name=1; Synonyms=Nogo-A, NI-220-250;  
 CC IsoId=Q9JK11-1; Sequence=Displayed;  
 CC Name=2; Synonyms=Nogo-B, Foocen-M1;  
 CC IsoId=Q9JK11-2; Sequence=VSP\_005658;  
 CC Name=3; Synonyms=Nogo-C, VP20;  
 CC IsoId=Q9JK11-3; Sequence=VSP\_005656, VSP\_005657;  
 CC Name=4; Synonyms=Foocen-M2;  
 CC IsoId=Q9JK11-4; Sequence=VSP\_005659;  
 CC -!- TISSUE SPECIFICITY: Isoforms 1, 2 and 3 are present in optic  
 CC nerve, spinal cord and cerebral cortex. Isoforms 1 and 2 are  
 CC present in dorsal root ganglion, sciatic nerve and PC12 cells  
 CC after longer exposure. Isoforms 2 and 3 are detected in kidney,  
 CC cartilage, skin, lung and spleen. Isoform 3 is expressed at high  
 CC level in skeletal muscle. In adult animals isoform 1 is expressed  
 CC mainly in the nervous system.  
 CC -!- SIMILARITY: Contains 1 reticulon domain.

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Db	227	:     :    :      :   :   :	286
Qy	285	EMGSSFSVSPKAESAVIVANPREEIIIVKNKDEEEKLVSNNILHXQQELPTALTCLKVKEDE	344
Db	287	EMGSSFKGSPKGESAILVENTKEEVIVRSKDKED-LVCSAALHSPQESPVG-----KEDR	340
Qy	345	VVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS-DMLAAGGKIESNLE	403
Db	341	VVSPEKTMDFNEMQMSVVPVREEYADFKPFEQAWEVKDTYEGSRDVLAA----RANVE	396
Qy	404	SKVDKKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIAT	463
Db	397	SKVDRKCLEDSEQKSLGKDESEGRNEDASFPSTPEPVKDSSRAYITCASFT-SATESTTA	455
Qy	464	NIFPILLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLT	523
Db	456	NTFPLEDHTSENKTDEKKIEERKAQIITEK-TSPKTSNPFLVAVQDSEADYVTTDTLSK	514
Qy	524	VTEEVVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLC	583
Db	515	VTEAAVSNMPEGLTPDLVQEACESELNEATGTKIAYETKVDLVQTSEAIQESLYPTAQLC	574
Qy	584	PSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEA-SSVNYESIKHEPENP	642
Db	575	PSFEEAEATPSPVLPDIVMEAPLNSLLPSAGASVVQPSVSPLEAPPPVSYDSIKLEPENP	634
Qy	643	PPYEEAMSVSLKVSGIKEEIKPENINAAQETEAPYISIACDLIKETKLSAEPAPDFSD	702
Db	635	PPYEEAMNVALKALGTKEGIKEPESFNAAVQETEAPYISIACDLIKETKLSTEPSDFSN	694
Qy	703	YSEMAKVEQVPDPHSELVEDSSPDSEPVDLFSDDSIPDVPQKQDETVMVLKESLTETSFE	762
Db	695	YSEIAKFEKSVPEHAELVEDSSPESEPVDLFSDDSIPEVPQTQEEAVMLMKESLTEVS-E	753
Qy	763	SMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELST	822
Db	754	TVAQHK-EERLSASPQELGKPYLESFQPNLHSTKDA-ASNDIPTLTKEKISLQMEEFNT	811
Qy	823	AVYSNDDLFISKEAQIRETETFSDDSSPIEIIDEFPTLISSKTDSFSKLAREYTDLEVSHK	882
Db	812	AIYSNDDLLSSKEDKIKESETFSDDSSPIEIIDEFPTFVSAKDDS-PKLAKEYTDLEVSDK	870
Qy	883	SEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATS SKVLLLPPDVSA	942
Db	871	SEIANIQSGADSLPCLELPCDLSFKNIYPK--DEVHVSDEFSENRSSVSKASISPSNVSA	928
Qy	943	LGHTQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKK	1002
Db	929	L-EPQTEMGSIVKSKSLTKEAEKKLPSDTEKEDRSLSAVLSAELSKTSVVDLLYWRDIKK	987
Qy	1003	TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAY	1062
Db	988	TGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAY	1047
Qy	1063	LESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFN	1122

Db 1048 LESEVAISEELVQKYSNSALGHVNSTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFN 1107

QY 1123 GLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE 1178  
 |||||:||||| |||||:|||||

Db 1108 GLTLLILALISLFSIPVIYERHQVQIDHYLGLANKSVKDAMAKIQAKIPGLKRKAD 1163

# RESULT 3

## RTN4\_MOUSE

ID RTN4\_MOUSE STANDARD; PRT; 199 AA.

AC Q99P72; Q9CTE3;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Reticulon 4 (Neurite outgrowth inhibitor) (Nogo protein).

GN RTN4 OR NOGO.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=3T3-L1; TISSUE=Adipocyte;

RA Coulson A.C., Craggs P.D., Morris N.J.;

RT "Mouse vp20/RTN4C cDNA.";

RL Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.

RN [2]

RP SEQUENCE OF 170-199 FROM N.A.

RC STRAIN=C57BL/6J; TISSUE=Embryo;

RX MEDLINE=21085660; PubMed=11217851;

RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,

RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

RA Lyons P., Marchionni L., Mashima J., Mazzearelli J., Mombaerts P.,

RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,

RA Hayashizaki Y.;

RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

CC -!- FUNCTION: Potent neurite outgrowth inhibitor which may also help

CC block the regeneration of the nervous central system in adults (By

CC similarity).

CC -!- SUBUNIT: Binds to RTN4R. Interacts with Bcl-x1 and Bcl-2 (By

CC similarity).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Anchored to the

CC membrane of the endoplasmic reticulum through 2 putative

```
CC      transmembrane domains (By similarity).
CC      -!- ALTERNATIVE PRODUCTS:
CC          Event=Alternative splicing; Named isoforms=1;
CC          Comment=A number of isoforms may be produced;
CC          Name=1;
CC          IsoId=Q99P72-1; Sequence=Displayed;
CC      -!- SIMILARITY: Contains 1 reticulon domain.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; AF326337; AAK08076.1; -.
DR      EMBL; AK003859; -; NOT_ANNOTATED_CDS.
DR      MGD; MGI:1915835; Rtn4.
DR      GO; GO:0005783; C:endoplasmic reticulum; IDA.
DR      GO; GO:0030176; C:integral to endoplasmic reticulum membrane; ISS.
DR      GO; GO:0005635; C:nuclear membrane; ISS.
DR      GO; GO:0005515; F:protein binding; ISS.
DR      GO; GO:0019987; P:negative regulation of anti-apoptosis; ISS.
DR      GO; GO:0030517; P:negative regulation of axon extension; ISS.
DR      GO; GO:0007399; P:neurogenesis; IDA.
DR      InterPro; IPR003388; Reticulon.
DR      Pfam; PF02453; Reticulon; 1.
DR      PROSITE; PS50845; RETICULON; 1.
KW      Endoplasmic reticulum; Alternative splicing; Transmembrane.
FT      DOMAIN           1         25        CYTOPLASMIC (Potential).
FT      TRANSMEM          26        50        POTENTIAL.
FT      DOMAIN           51       137        LUMENAL (Potential).
FT      TRANSMEM         138       162        POTENTIAL.
FT      DOMAIN          163       199        CYTOPLASMIC (Potential).
FT      DOMAIN           12       199        RETICULON.
SQ      SEQUENCE    199 AA;  22466 MW;  07BE5D580059ED9C CRC64;

Query Match              15.4%; Score 915; DB 1; Length 199;
Best Local Similarity   97.4%; Pred. No. 4.9e-29;
Matches 186; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      988 KTSVVDLLYWDRDIKKTGVVFASLFLLLSTLVFSIVSVTAYIALALLSVTISFRIYKGVI 1047
Db            | |||||
          9 KDKVVDLLYWDRDIKKTGVVFASLFLLLSTLVFSIVSVTAYIALALLSVTISFRIYKGVI 68

QY      1048 QAIQKSDEGHPFRAYLESEVAISEELVQKYNSALGHVNCTIKELRRLFLVDDLVDLSLK 1107
Db            | |||||
          69 QAIQKSDEGHPFRAYLESEVAISEELVQKYNSALGHVNSTIKELRRLFLVDDLVDLSLK 128

QY      1108 AVLMMWFPTYVGALFNGLTLLILALISLFSVPVIYERHQAQIDHYLGANKNVKDAMAKIQ 1167
Db            | |||||
          129 AVLMMWFPTYVGALFNGLTLLILALISLFSIPVIYERHQAQIDHYLGANKSVKDAMAKIQ 188

QY      1168 AKIPGLKRKAE 1178
Db            | |||||
          189 AKIPGLKRKAE 199
```

RESULT 4

RTN1\_RAT

ID RTN1\_RAT STANDARD; PRT; 777 AA.  
AC Q64548; Q64547;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Reticulon 1 (Neuroendocrine-specific protein) (S-rex).  
GN RTN1 OR NSP.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORMS RTN1-B AND RTN1-S).  
RC STRAIN=Wistar; TISSUE=Brain cortex;  
RX MEDLINE=96386034; PubMed=8793864;  
RA Baka I.D., Ninkina N.N., Pinon L.G.P., Adu J., Davies A.M.,  
RA Georgiev G.P., Buchman V.L.;  
RT "Intracellular compartmentalization of two differentially spliced s-  
RT rex/NSP mRNAs in neurons.";  
RL Mol. Cell. Neurosci. 7:289-303(1996).  
CC -!- FUNCTION: May be involved in neuroendocrine secretion or in  
CC membrane trafficking in neuroendocrine cells.  
CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum membrane (By  
CC similarity).  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=RTN1-B; Synonyms=S-RexB;  
CC IsoId=Q64548-1; Sequence=Displayed;  
CC Name=RTN1-S; Synonyms=S-RexS;  
CC IsoId=Q64548-2; Sequence=VSP\_005647, VSP\_005648;  
CC -!- TISSUE SPECIFICITY: EXPRESSED PREDOMINANTLY IN CENTRAL AND  
CC PERIPHERAL NERVOUS SYSTEM OF NEWBORN AND ADULT RATS. LOW LEVELS  
CC HAVE BEEN ALSO DETECTED IN HEART, ADRENAL GLAND AND SPLEEN.  
CC EXPRESSION OF ISOFORM RTN1-B IS RESTRICTED TO PARTICULAR NEURONAL  
CC TYPES.  
CC -!- DEVELOPMENTAL STAGE: DETECTED ON EMBRYONIC DAY E10 IN THE  
CC HINDBRAIN AND IN E11 IN THE FOREBRAIN. DURING THE NEXT 3 EMBRYONIC  
CC DAYS THE LEVELS OF S-REXS INCREASES AND REMAINS STABLE AT E13 IN  
CC THE HINDBRAIN AND AT E14 IN THE FOREBRAIN. THE LEVELS OF S-REXB  
CC DOES NOT CHANGE AS SIGNIFICANTLY DURING DEVELOPMENT OF THE  
CC HINDBRAIN.  
CC -!- SIMILARITY: Contains 1 reticulon domain.  
CC -----  
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CC -----  
DR EMBL; U17604; AAC53046.1; -.  
DR EMBL; U17603; AAC53045.1; -.





RA Ramaekers F.C.S., Van de Ven W.J.M.;  
 RT "Cloning and expression of alternative transcripts of a novel  
 RT neuroendocrine-specific gene and identification of its 135-kDa  
 RT translational product.";  
 RL J. Biol. Chem. 268:13439-13447(1993).  
 RN [2]  
 RP ALTERNATIVE SPLICING.  
 RX MEDLINE=96429995; PubMed=8833145;  
 RA Roebroek A.J.M., Ayoubi T.A.Y., Van de Velde H.J.K.,  
 RA Schoenmakers E.F.P.M., Pauli I.G.L., Van de Ven W.J.M.;  
 RT "Genomic organization of the human NSP gene, prototype of a novel gene  
 RT family encoding reticulons.";  
 RL Genomics 32:191-199(1996).  
 RN [3]  
 RP TISSUE SPECIFICITY.  
 RX MEDLINE=98228245; PubMed=9560466;  
 RA Hens J., Nuydens R., Geerts H., Senden N.H., Van de Ven W.J.M.,  
 RA Roebroek A.J., van de Velde H.J.K., Ramaekers F.C., Broers J.L.;  
 RT "Neuronal differentiation is accompanied by NSP-C expression.";  
 RL Cell Tissue Res. 292:229-237(1998).  
 CC -!- FUNCTION: May be involved in neuroendocrine secretion or in  
 CC membrane trafficking in neuroendocrine cells.  
 CC -!- SUBCELLULAR LOCATION: Endoplasmic reticulum membrane.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Name=RTN1-A; Synonyms=NSP-A;  
 CC IsoId=Q16799-1; Sequence=Displayed;  
 CC Name=RTN1-B; Synonyms=NSP-B;  
 CC IsoId=Q16799-2; Sequence=VSP\_005644;  
 CC Name=RTN1-C; Synonyms=NSP-C;  
 CC IsoId=Q16799-3; Sequence=VSP\_005645, VSP\_005646;  
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN NEURAL AND NEUROENDOCRINE TISSUES  
 CC AND CELL CULTURES DERIVED THEREFROM. EXPRESSION OF ISOFORM RTN1-C  
 CC IS STRONGLY CORRELATED WITH NEURONAL DIFFERENTIATION.  
 CC -!- PTM: Isoforms RTN1-A and RTN1-B are phosphorylated.  
 CC -!- SIMILARITY: Contains 1 reticulon domain.  
 CC -----  
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 CC -----  
 DR EMBL; L10333; AAA59950.1; -.  
 DR EMBL; L10334; AAA59951.1; -.  
 DR EMBL; L10335; AAA59952.1; -.  
 DR PIR; A46583; A46583.  
 DR PIR; I60904; I60904.  
 DR Genew; HGNC:10467; RTN1.  
 DR MIM; 600865; -.  
 DR GO; GO:0030176; C:integral to endoplasmic reticulum membrane; TAS.  
 DR GO; GO:0004871; F:signal transducer activity; NAS.  
 DR GO; GO:0030182; P:neuron differentiation; TAS.  
 DR GO; GO:0007165; P:signal transduction; NAS.  
 DR InterPro; IPR003388; Reticulon.

DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS50845; RETICULON; 1.  
 KW Endoplasmic reticulum; Alternative splicing; Transmembrane;  
 KW Phosphorylation.  
 FT TRANSMEM 603 623 POTENTIAL.  
 FT TRANSMEM 726 746 POTENTIAL.  
 FT DOMAIN 589 776 RETICULON.  
 FT DOMAIN 609 612 POLY-LEU.  
 FT VARSPLIC 1 420 Missing (in isoform RTN1-B).  
 FT /FTId=VSP\_005644.  
 FT VARSPLIC 1 568 Missing (in isoform RTN1-C).  
 FT /FTId=VSP\_005645.  
 FT VARSPLIC 569 588 GPGPLGPGAPPPLLFLNKQK -> MQATADSTKMDCVWSNW  
 FT KSQ (in isoform RTN1-C).  
 FT /FTId=VSP\_005646.  
 SQ SEQUENCE 776 AA; 83617 MW; CASB6232353096FE CRC64;

Query Match 13.3%; Score 787.5; DB 1; Length 776;  
 Best Local Similarity 31.9%; Pred. No. 2e-23;  
 Matches 229; Conservative 91; Mismatches 190; Indels 207; Gaps 25;

QY 588 ESEATPSPVLPDI--VMEAPLNSA-----VPSAGASVIQPS SSPLE---ASSVNY---- 632  
 | ||| |||: : | |: | : : ||: | : |  
 Db 141 EELGTPGPSLPDVPGIESRGLFSSDSGIEMTPAESTEVNKKILADPLDQMKAEAYKYIDIT 200  
 QY 633 --ESIKHEPENPPPYEEA-----MSVSLKVSGIKKEIKEPENINAAL-----QET 675  
 | :||: :: | |: :|| |::| | | : : |  
 Db 201 RPEEVKHQEQHHPELEDKDLDFKNKDTDISIKPEGVREPDK-PAPVEGKIIKDHLLEEST 259  
 QY 676 EAPYISIIACDL-----IKETKLSAEPAPDFSDYSEMAKVEQVPDPHSELVED 722  
 |||| || :| | ||: : :: | : :  
 Db 260 FAPYID---DLSEEQRRAPOITTPVKITLLEIEPSVE-----TTTQEKTPKQDICLK 309  
 QY 723 SSPDSEPVDLFS---DDS-----IPDVPQKQ-----DETVMVLVKESLTETSF 761  
 |||: | | || | : | || : ||:  
 Db 310 PSPDTVPTVTVSEPEDDSPGSITPPSSGTEPSAAESQGKGSISEDELITAIKEA----- 363  
 QY 762 ESMIEYENKEKLSALPPEGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELS 821  
 : || | : : | || | || : :  
 Db 364 -KGLSYETAENPRPVGQLADRP-----EVKARSGPPTIPSPLDHEA 403  
 QY 822 TAVYSNDDLFISKEAQIRETETFS DSSPIEIIIDFP---TLISSKTDSFS----- 868  
 :: | | | ||: | | : | ||  
 Db 404 SSAESGD-----SEIELVSEDPMMAEDALPSGYVSFGHVGGPPPPSP 444  
 QY 869 -----KLAREYTDLEVSHKSEIANAPDGAGSLPCTELPHDLSLKNIQPKVEEKISFSD 921  
 : || : |: : | : : | : || | | | |  
 Db 445 ASPSIQYSILREEREAE L DSELIIESCDASSAS-----EESPKREQDSPPMKPSALD 496  
 QY 922 DF-----SKNGSATS K VLL-----LPPDVSA LGHTQAEIESIVKP 956  
 | : | | | || | || | : : |  
 Db 497 AIREETGVRAEERAPSRRGLAEPGSFLDYPSTEPQGPPELPPGDGAL-----EPETPMLP 551  
 QY 957 KVLEKEAEKKLPDTEKEDRSPSA-----IFSADLGKTSVVDLLYWRDIK 1001  
 : | : : ||: | : | | : |||||  
 Db 552 -----RKPEEDSSSNQSPAATKGPGLGPGAPPPLL F---LNKQKAIDLLYWRDIK 599



Qy	1002	KTGVVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRA	1061
		:  :    :             :      :               :  :  :     :	
Db	600	QTGIVFGSFLLLLFSLTQFSVVSVMAYLALAALSATISFRIYKSVLQAVQKTDEGHPFKA	659
Qy	1062	YLESEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALF	1121
		: :  :  :   : :    :                   :	
Db	660	YLELEITLSQEIQKYTDCLQFYVNSTLKELRRLFLVQDLVDLSLKFAVLMWLLTYVGALF	719
Qy	1122	NGLTLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGLKRKAE	1178
		: : : : : :   :           :  :	
Db	720	NGLTLLLMVVSMFTLPVVYVKHQAQIDQYLGLVRTHINAVVAKIQAKIPGAKRHAE	776

RESULT 6

```

RTN3_MOUSE
ID   RTN3_MOUSE          STANDARD;          PRT;          237 AA.
AC   Q9ES97;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Reticulon protein 3.
GN   RTN3.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Huang X., Zhou Y., Qiang H., Yuan J., Qiang B.;
RT   "Cloning and expression profile of a novel mouse cDNA encoding a human
RT   RTN3 homolog.";
RL   Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic

```

CC       reticulum (Potential).  
 CC    -!- SIMILARITY: Contains 1 reticulon domain.  
 CC    -----  
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 CC    -----  
 DR    EMBL; AF195940; AAG31360.1; -.  
 DR    EMBL; BC014697; AAH14697.1; -.  
 DR    MGD; MGI:1339970; Rtn3.  
 DR    InterPro; IPR003388; Reticulon.  
 DR    Pfam; PF02453; Reticulon; 1.  
 DR    PROSITE; PS50845; RETICULON; 1.  
 KW    Transmembrane; Endoplasmic reticulum.  
 FT    TRANSMEM       69       89       POTENTIAL.  
 FT    TRANSMEM       167      187      POTENTIAL.  
 FT    DOMAIN         49      237      RETICULON.  
 SQ    SEQUENCE    237 AA;   25428 MW;   EB60A0A7AC45F0DE CRC64;

Query Match                   10.6%; Score 626; DB 1; Length 237;  
 Best Local Similarity       53.2%; Pred. No. 6.9e-18;  
 Matches 125; Conservative   41; Mismatches 53; Indels 16; Gaps 4;

Qy       960 EKEAEKKLPS-DTEKEDRSPSAIFSAD-----LGKTS-----VVDLLYWRDIKKTG 1004  
           | | : | | :       | | | :       | | |       | | : | | : | | |  
 Db       3 ESSAATQSPSVSSSSSGAEPALGGGGGSPGACPALGAKSCGSSCAVHDLIFWRDVKKTG 62  
  
 Qy       1005 VVFGASLFLLLSLTVFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLE 1064  
           | | | : | : | | | | | : | | : | : | | | | | | | | | | | : | | : | | : | | : | | :  
 Db       63 FVFGTTLIMLLSLAAFSVISVVSYLILALLSVTISFRVYKSVIAVQKSEEGHPFKAYLD 122  
  
 Qy       1065 SEVAISEELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGL 1124  
           : : : | |       | | : | : | | : | : | | | | | | | | | | | : | | : | | : | | :  
 Db       123 VDITLSSEAFHNYMNAAMVHVNKALKLIIRLFLVEDLVDLSLKLAVFMWLMTYVGAVFNGI 182  
  
 Qy       1125 TLLILALISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGL-KRKAE 1178  
           | | | | | : : | | | : | | : | : | | | | | | | | | : | | : | | : | | : | | :  
 Db       183 TLLILAE LLVFSVPVIVYEKYKTQIDHYVGIARDQTKSIVEKIQAKLPGI AKKKAE 237

# RESULT 7

RTN3\_HUMAN

ID   RTN3\_HUMAN       STANDARD;       PRT;   236 AA.

AC   O95197;

DT   16-OCT-2001 (Rel. 40, Created)

DT   16-OCT-2001 (Rel. 40, Last sequence update)

DT   10-OCT-2003 (Rel. 42, Last annotation update)

DE   Reticulon protein 3 (Neuroendocrine-specific protein-like 2) (NSP-like  
 DE   protein II) (NSPLII).

GN   RTN3 OR NSPL2.

OS   Homo sapiens (Human).

OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.  
 RC TISSUE=Retina;  
 RX MEDLINE=99265974; PubMed=10331947;  
 RA Moreira E.F., Jaworski C.J., Rodriguez I.R.;  
 RT "Cloning of a novel member of the reticulon gene family (RTN3): gene  
 RT structure and chromosomal localization to 11q13.";  
 RL Genomics 58:73-81(1999).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Huang X., Zhou Y., Du G., Yuan J., Qiang B.;  
 RT "Cloning and expression analysis of a cDNA encoding a novel  
 RT neuroendocrine-specific protein-like protein 1: NSPL1.";  
 RL Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain, Eye, and Lymph;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic  
 CC reticulum (Potential).  
 CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED WITH HIGHEST EXPRESSION IN  
 CC BRAIN. THREE TIMES MORE ABUNDANT IN MACULA THAN IN PERIPHERAL  
 CC RETINA.  
 CC -!- SIMILARITY: Contains 1 reticulon domain.  
 CC -----  
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 CC -----  
 DR EMBL; AF059524; AAC99319.1; -.  
 DR EMBL; AF059529; AAD20951.1; -.  
 DR EMBL; AF059525; AAD20951.1; JOINED.

DR EMBL; AF059526; AAD20951.1; JOINED.  
 DR EMBL; AF059527; AAD20951.1; JOINED.  
 DR EMBL; AF059528; AAD20951.1; JOINED.  
 DR EMBL; AF119297; AAD26810.1; -.  
 DR EMBL; BC000634; AAH00634.1; -.  
 DR EMBL; BC010556; AAH10556.1; -.  
 DR EMBL; BC011394; AAH11394.1; -.  
 DR EMBL; BC022993; AAH22993.1; -.  
 DR Genew; HGNC:10469; RTN3.  
 DR MIM; 604249; -.  
 DR GO; GO:0005615; C:extracellular space; TAS.  
 DR InterPro; IPR003388; Reticulon.  
 DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS50845; RETICULON; 1.  
 KW Transmembrane; Endoplasmic reticulum.  
 FT TRANSMEM 68 88 POTENTIAL.  
 FT TRANSMEM 177 197 POTENTIAL.  
 FT DOMAIN 48 236 RETICULON.  
 SQ SEQUENCE 236 AA; 25609 MW; DDC6A4544ABCDFB7 CRC64;

Query Match 10.6%; Score 625.5; DB 1; Length 236;  
 Best Local Similarity 54.8%; Pred. No. 7.1e-18;  
 Matches 119; Conservative 41; Mismatches 56; Indels 1; Gaps 1;

Qy 963 AEKKLPSTDEKEDRSPSAIFSADLGKTSVVDLLYWRIKKTGVVFGASLFLLLSLTVFSI 1022  
 || | : : : ||::|||:|||| ||| :| :||| ||:  
 Db 20 AEPSAPGGGGSPGACPALGTKSCSSSCAVHDLIFWRDVKKTGFVFGTTLIMLLSLAAFSV 79  
  
 Qy 1023 VSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISEELVQKYSNSAL 1082  
 :|| :| : ||||| ||||| ||||:||||:||||: : :| | | :| :|:  
 Db 80 ISVVSYLILALLSVTISFRIYKSVIQAVQKSEEGHPFKAYLDVDITLSSEAFHNYMNAAM 139  
  
 Qy 1083 GHVNCTIKELRRLFLVDDLVDLSLKFAVLMMWVFTYVGFALFNGLTLLILALISLFSVPVIYE 1142  
 |:| :| : |||||:||||| || ||: ||||:||||:||||| : :|||:|:  
 Db 140 VHINRALKLIIRLFLVEDLVDLSLKLAVFMWLMTYVGVAFNGITLLILAELLIFSVPIVYE 199  
  
 Qy 1143 RHQAQIDHYLGLANKNVKDAMAKIQAKIPGL-KRKAE 1178  
 ::: |||||:|:| | : |||||:|:| |:|  
 Db 200 KYKTQIDHYVGIARDQTKSIVEKIQAKLPGIAKKKAE 236

# RESULT 8

## RTN2\_HUMAN

ID RTN2\_HUMAN STANDARD; PRT; 545 AA.  
 AC 075298; 060509;  
 DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Reticulon protein 2 (Neuroendocrine-specific protein-like 1) (NSP-like  
 DE protein 1) (NSPLI).  
 GN RTN2 OR NSPL1.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A., ALTERNATIVE SPLICING, AND TISSUE SPECIFICITY.

RC TISSUE=Lung carcinoma;  
 RX MEDLINE=98360096; PubMed=9693037;  
 RA Roebroek A.J.M., Contreras B., Pauli I.G.L., Van de Ven W.J.M.;  
 RT "cDNA cloning, genomic organization, and expression of the human RTN2  
 RT gene, a member of a gene family encoding reticulons.";  
 RL Genomics 51:98-106(1998).  
 RN [2]  
 RP SEQUENCE OF 108-545 FROM N.A. (ISOFORM RTN2-B).  
 RC TISSUE=Brain;  
 RX MEDLINE=98191726; PubMed=9530622;  
 RA Geisler J.G., Stubbs L.J., Wasserman W.W., Mucenski M.L.;  
 RT "Molecular cloning of a novel mouse gene with predominant muscle and  
 RT neural expression.";  
 RL Mamm. Genome 9:274-282(1998).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein. Endoplasmic  
 CC reticulum (Potential).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=RTN2-A;  
 CC IsoId=O75298-1; Sequence=Displayed;  
 CC Note=Isoform RTN2-C is produced by alternative initiation at  
 CC Met-341 of isoform RTN2-A;  
 CC Name=RTN2-B;  
 CC IsoId=O75298-2; Sequence=VSP\_005649;  
 CC Event=Alternative initiation;  
 CC Comment=2 isoforms, RTN2-A (shown here) and RTN2-C, are produced  
 CC by alternative initiation at Met-1 and Met-341;  
 CC -!- TISSUE SPECIFICITY: ISOFORM RTN2-C IS HIGHLY EXPRESSED IN SKELETAL  
 CC MUSCLE.  
 CC -!- SIMILARITY: Contains 1 reticulon domain.  
 CC -----  
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 CC -----  
 DR EMBL; AF004222; AAC32542.1; -.  
 DR EMBL; AF004223; AAC32543.1; -.  
 DR EMBL; AF004224; AAC32544.1; -.  
 DR EMBL; AF038540; AAC14910.1; -.  
 DR Genew; HGNC:10468; RTN2.  
 DR MIM; 603183; -.  
 DR GO; GO:0030176; C:integral to endoplasmic reticulum membrane; NAS.  
 DR GO; GO:0004871; F:signal transducer activity; NAS.  
 DR GO; GO:0007165; P:signal transduction; NAS.  
 DR InterPro; IPR003388; Reticulon.  
 DR Pfam; PF02453; Reticulon; 1.  
 DR PROSITE; PS50845; RETICULON; 1.  
 KW Endoplasmic reticulum; Alternative splicing; Transmembrane;  
 KW Alternative initiation.  
 FT CHAIN 1 545 RETICULON PROTEIN 2, ISOFORM RTN2-A.  
 FT CHAIN 341 545 RETICULON PROTEIN 2, ISOFORM RTN2-C.  
 FT INIT\_MET 341 341 FOR ISOFORM RTN2-C.  
 FT TRANSMEM 368 388 POTENTIAL.

FT TRANSMEM 463 483 POTENTIAL.  
 FT DOMAIN 345 545 RETICULON.  
 FT VARSPLIC 272 344 Missing (in isoform RTN2-B).  
 FT /FTId=VSP\_005649.  
 SQ SEQUENCE 545 AA; 59263 MW; 971FD2F909E1E9E6 CRC64;

Query Match 8.7%; Score 514; DB 1; Length 545;  
 Best Local Similarity 28.2%; Pred. No. 3.7e-13;  
 Matches 169; Conservative 81; Mismatches 186; Indels 164; Gaps 18;

```

Qy      676 EAPYISIACDLIKETKLSAEPAPDFSDYSEMAKVEQPVPDHSELVEDSSPD-SEPVDL-F 733
      |||      | | | | | : | : | : | | | | | : | |
Db      13 EAP-----STASSTPDSTEGGNDDSFRELHTAREFSEED--ETTSQDWGTPRELTF 64

Qy      734 S-----DDSI PDVPQKQDET VMLVKESLTETSFESMIEYENKEKLSALPPEG 780
      |      | | | | | : | : | : | : | | | | |
Db      65 SYIAFDGVVGSGGRRDSTARRPRPQGRSVSEPRDQHPQPSLGSLESIPSLSQSPEPGRR 124

Qy      781 GKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFISKEAQIRE 840
      | |      | | | | | : | : : | | : : : |
Db      125 GDP-----DTAPPSE---RPLEDLRLRLDHLG-----WVARGTGSGE 158

Qy      841 TETFSDSPIEIIIDEFPTLISSKTD SFSKLAREYTDLEVSHKSEIANAPDGAGSLPCTEL 900
      : | | : : | | | : | | | | | | | | | |
Db      159 DSSTSSSTPLE--DEEP-----QEPNRLETGEAGE-----EL 188

Qy      901 PHDLSLKNIQPKVEEKI-----SFSDDFSKNGSATS KVL LPPDV SALGHT 946
      || : | | | : : | | : : : : | | : |
Db      189 --DLRLRLAQPSPEVLTPQLSPGSGTPQAGTPSPSRSDSNSGPEEPLLEEEKQWGPL 246

Qy      947 QAE-----IESIVKPKVLEKEAE-----KKLP----- 968
      : | : | : | : | : | : | : | : |
Db      247 EREPVRGQCLDSTDQLEFTVEPRLLGTAMEWLKTSLLLAVYKTVPILELSPPLWTAIGWV 306

Qy      969 -----SDTEKEDRSPSAIFSADLGKTSVVDLLYWRDIKKTGVVFGASL 1011
      : : : | | | : | | | : | : | : |
Db      307 QRGPTPTPTVLRVLLKWAKSPRSSGVPSLSLGADMG-SKVADLLYWKDTRTSGVFTGLM 365

Qy      1012 FLLLSLT VFSIVSVTAYIALALLSVTISFRIYKGVIAIQKSDEGHPFRAYLESEVAISE 1071
      | | | | | | | : : | | | | : : | : : | : : :
Db      366 VSL LCL LHFSIVSVA AHLAL LLLCGTISLRVYRKVLQAVHRGDGANPFQAYLDVDLTLTR 425

Qy      1072 ELVQKYSNSALGHVNCTIKELRRLFLVDDLVDLSLKFAVLMWVFTYVGALFNGLTLLILAL 1131
      | : : | : | : | | | : | : | : | : | : | :
Db      426 EQTERLSHQITSRVVSAATQLRHFFLVEDLVDLSKLALLFYILTFVGAIFNGLTLLILGV 485

Qy      1132 ISLFSVPVIYERHQAQIDHYLGLANKNVKDAMAKIQAKIPGL-----KRKAE 1178
      | | : : : : | : | | | : | : | : | : | | |
Db      486 IGLFTIPLLYRQHQAQIDQYVGLVTNQLSHIKAKIRAKIPGTGALASAAA VSGSKAKAE 545

```

RESULT 9

RTN2\_MOUSE

ID RTN2\_MOUSE STANDARD; PRT; 471 AA.

AC 070622; 070620;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)  
 DE Reticulon protein 2 (Neuroendocrine-specific protein-like 1) (NSP-like  
 DE protein 1) (NSPLI).  
 GN RTN2 OR NSPL1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND TISSUE SPECIFICITY.  
 RC STRAIN=FVB/N, and 129/Sv; TISSUE=Cerebellum, and Skeletal muscle;  
 RX MEDLINE=98191726; PubMed=9530622;  
 RA Geisler J.G., Stubbs L.J., Wasserman W.W., Mucenski M.L.;  
 RT "Molecular cloning of a novel mouse gene with predominant muscle and  
 RT neural expression.";  
 RL Mamm. Genome 9:274-282(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Retina;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 CC -!- SUBCELLULAR LOCATION: Membrane-bound. Endoplasmic reticulum  
 CC (Potential).  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=2;  
 CC Name=1; Synonyms=Brain;  
 CC IsoId=070622-1; Sequence=Displayed;  
 CC Name=2; Synonyms=Muscle;  
 CC IsoId=070622-2; Sequence=VSP\_005650, VSP\_005651;  
 CC -!- TISSUE SPECIFICITY: Expressed predominantly in neural and muscular  
 CC tissues.  
 CC -!- SIMILARITY: Contains 1 reticulon domain.  
 CC -----  
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Qy 1128 ILALISLFSVPVIYERHQAIQIDHYLGLANKNVKDAMAKIQAKIPGL-----KR 1175  
 || ::||:|:|:| :| | | | | | :| | : | | | | | | |  
 Db 409 ILGVVALFTVPLLYRQHQAQIDQYVGLVTNQLSHIKAKIRAKIPGTGTLAPTASVSGSKA 468

Qy 1176 KAE 1178  
 |||  
 Db 469 KAE 471

RESULT 10

CPN\_DROME

ID CPN\_DROME STANDARD; PRT; 865 AA.

AC Q02910;

DT 01-OCT-1993 (Rel. 27, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)

DT 10-OCT-2003 (Rel. 42, Last annotation update)

DE Calphotin.

GN CPN OR CAP.

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI\_TaxID=7227;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Canton-S;

RX MEDLINE=93165729; PubMed=8094559;

RA Martin J.H., Benzer S., Rudnicka M., Miller C.A.;

RT "Calphotin: a Drosophila photoreceptor cell calcium-binding protein.";

RL Proc. Natl. Acad. Sci. U.S.A. 90:1531-1535(1993).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=Canton-S;

RX MEDLINE=93165730; PubMed=8434015;

RA Ballinger D.G., Xue N., Harshman K.D.;

RT "A Drosophila photoreceptor cell-specific protein, calphotin, binds

RT calcium and contains a leucine zipper.";

RL Proc. Natl. Acad. Sci. U.S.A. 90:1536-1540(1993).

CC -!- FUNCTION: Might function as a calcium-sequestering "sponge" to  
 CC regulate the amount of free cytoplasmic calcium. It binds 0.3 mole  
 CC of Ca(2+) per mole of protein.

CC -!- SUBUNIT: Homodimer (Probable).

CC -!- SUBCELLULAR LOCATION: Cytoplasmic; hypodense compartment.

CC -!- TISSUE SPECIFICITY: Soma and axons of photoreceptor cells of  
 CC compound eyes and ocelli.

CC -!- DEVELOPMENTAL STAGE: Expressed early in photoreceptor cell  
 CC development.

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 CC -----

DR EMBL; L02111; AAA28405.1; -.  
 DR EMBL; L05080; AAA28420.1; -.  
 DR PIR; A47282; A47282.  
 DR PIR; A47283; A47283.  
 DR FlyBase; FBgn0010218; Cpn.  
 DR GO; GO:0005509; F:calcium ion binding; IDA.  
 KW Calcium-binding.  
 FT CONFLICT 36 36 A -> AVAPAVVA (IN REF. 2).  
 FT CONFLICT 43 43 I -> T (IN REF. 2).  
 FT CONFLICT 64 64 I -> V (IN REF. 2).  
 FT CONFLICT 76 76 T -> A (IN REF. 2).  
 FT CONFLICT 100 100 P -> PP (IN REF. 2).  
 FT CONFLICT 126 127 VQ -> AP (IN REF. 2).  
 FT CONFLICT 154 154 I -> V (IN REF. 2).  
 FT CONFLICT 160 160 S -> T (IN REF. 2).  
 FT CONFLICT 534 534 A -> E (IN REF. 2).  
 FT CONFLICT 699 699 I -> T (IN REF. 2).  
 FT CONFLICT 703 703 V -> L (IN REF. 2).  
 FT CONFLICT 721 721 D -> E (IN REF. 2).  
 SQ SEQUENCE 865 AA; 84781 MW; 2110417E0B0E7CFE CRC64;

Query Match 5.5%; Score 324.5; DB 1; Length 865;  
 Best Local Similarity 22.3%; Pred. No. 1.1e-05;  
 Matches 229; Conservative 128; Mismatches 375; Indels 297; Gaps 49;

Qy 59 PAAGLSAAPVPTAPAAGAPLMDFGNDFVPPAPRGPLPAAPPVAPERQPSWDSPVSSSTVP 118  
 | : ||| | | ||: | || | : | | | : | : |  
 Db 9 PVSAPVAAPV-TPSAVAAPVQVVSPAAVAPAPAAPIAVTPVAPPPTLASVQPATV--TIP 65

Qy 119 APSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQAEPVWTPPAP----APAAPP--ST 172  
 ||:|:|:|:|:| | | ||: || : || | | || | : |  
 Db 66 APAPIAAASVTP---VASVAPPVVAAPTTPAA-SPVSTPVAVAQIPVAVSAPVAPPVAAAT 121

Qy 173 PAAPKRRGSSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLETAASXPSLSPLSAASF 232  
 | : : | : | | | : | : | : | : | : | : |  
 Db 122 PTPVVQIPVAAPVIAT-----PPVAASA-----PT----PAAVTPVISPVIAS-- 160

Qy 233 KEHEYLGNLSTVLPTTEGTLQENVSEASKEVSEKAKTLLIDRDLTEFSELEYSEMGSSFSV 292  
 | : | | | : : | : : | : | : | : | : | : |  
 Db 161 -----PPVVPANTT----VPVAAPVAAPVAAPVVPVAPVLAP-----AV 194

Qy 293 SPKAESAVIVAN-----PREEIIIVKNKDEEEKLVSNILHXQQELPTALTKLVKEDEVVS 347  
 : | : | : | | | | : | : | : | : | : | : |  
 Db 195 APAV--APVVAETPAPPPVAEIPVAT-----IPECVAPLIPEVSVVA 234

Qy 348 SEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDSDMLAAGGKIESNLESKVD 407  
 : | : | | | | | | : | : | : | : | : | : |  
 Db 235 T---KPLAAEPVVVAPPATET-----PVVAPAAASPHVSVAPAVETAVVAPVS 280

Qy 408 KKCFAADSLEQTNHEKDSESSNDDTSFPSTPEGIKDRSGAYITCAPFNPAATESIATNIFP 467  
 | | : : | : | | | |  
 Db 281 -----ASTEPPV--AAATLTAPETPAL----- 301

Qy 468 LLEDPTSENXTDEKKIEEKKQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTEE 527  
 | : | | | | | | | |  
 Db 302 -----APVVAESQ-----VAA-----NTVVATPP 320

Qy 528 VVANMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSSEVMQESLYPA----- 579  
 | | : | : | : | | : | | : | | : | |  
 Db 321 TPAPEPETIAPPVV-----AETPEVASVAVA-ETTPPVV--PPVAAESI-PAPVVATTPV 371

Qy 580 -AQLCPSFEESEATPSPVLPDIVMEAPLNSAVPSAGASVIQSSSPLEASSVNYESIKHE 638  
 | | : : | : | | : : : | | : | : | :  
 Db 372 PATLAVTDPDVTASAVPELPPVIAPSVPVSAVAETPVDLAPPVLPVAAEPVPAVVAEET 431

Qy 639 PENPPPYEEAMSV-SLKVSGIKEEIKEPENINAALQETEAPYISACDLIKETKLSAEP 697  
 | | | | : : : | : : | | : | | : | : : | |  
 Db 432 PETPAPASAPVTIAALDIPEVAPVIAAPSDAPAEAPSAAPIVSTPPTTASVPETTAPPA 491

Qy 698 P-----DFSDYSEMAKVEQVPVDHSEL-----VEDSSPDSEPVDLFSDDSI--DVPQK 744  
 | | | | : | | | : | | : | | : | | : | |  
 Db 492 AVPTEPIDVSVLSE-AAIETPVAPPVEVTTEVAVADVAPPEAAADLIIEPVEPPAPIPDL 550

Qy 745 QDETVMLVKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEV 804  
 : | : : | : : : | : | : : : | : : : |  
 Db 551 LEQTTSVPAVEAAESTSSPIPE-----TSLPPPNEAVASPEVAVAPITAPEPIPEPEP 603

Qy 805 STLSKKEKIPLQ---MEELSTAVYSNDDLFISKEAQIRETETFSDDSPIEIIDFPTLI 860  
 | : | | : : : | | | : | | | | | :  
 Db 604 SLATPTEPIPVVEAPVVIQEAVDV-----EVPVTETST---SIP-ETTVEFPEAV 649

Qy 861 SSKTDSFSKLAREYTDLEV-SHKSEIANAPDGAGSLPCTELP-----HDL 906  
 : | | : | : : : | | | : | : : : :  
 Db 650 AEKV-----LDPATEAPVTTQEPDVANINDGA---PATEITTPAVEIVTAAAEVSDIAI 701

Qy 907 KNIQPKVEEKISFSDDFSKNGSATSKVLL----LP-----PDVSALG----- 944  
 | | | : : : : : : : : : : : : : :  
 Db 702 PVIDPPVPQEIAVA-EIPETDTKPAEVIVEQSTIPIEAPVPEVSKYAEPVISEAPAAEVP 760

Qy 945 -----HTQAEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSADLGKTSVVDLLY 996  
 : | | : | | : | | : | : : | | | : | : | |  
 Db 761 ITAGDNPNTSVGISEVV-PTIAEKPVEEVPTSEIPEQSSSPSD--SVPVAK--ITPLL- 814

Qy 997 WRDIKKTGV 1005  
 | | : | |  
 Db 815 -RDLQTTDV 822

RESULT 11

PCLO\_HUMAN

ID PCLO\_HUMAN STANDARD; PRT; 5147 AA.  
 AC Q9Y6V0; O43373; O60305; Q9BVC8; Q9UIV2; Q9Y6U9;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Piccolo protein (Aczonin) (Fragments).  
 GN PCLO OR ACZ OR KIAA0559.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE OF 1-759 FROM N.A.  
 RC TISSUE=Brain;

RX MEDLINE=99439764; PubMed=10508862;  
 RA Wang X., Kibschull M., Laue M.M., Lichte B., Petrasch-Parwez E.,  
 RA Kilimann M.W.;  
 RT "Aczonin, a 550-kd putative scaffolding protein of presynaptic active  
 RT zones, shares homology regions with rim and bassoon and binds  
 RT profilin.";  
 RL J. Cell Biol. 147:151-162(1999).  
 RN [2]  
 RP SEQUENCE OF 552-4404 FROM N.A.  
 RA Kraemer J., Wollam C., Wohldmann P., McGrane B.;  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP SEQUENCE OF 3619-5147 FROM N.A. (ISOFORM 2).  
 RC TISSUE=Brain;  
 RX MEDLINE=98290545; PubMed=9628581;  
 RA Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,  
 RA Nomura N., Ohara O.;  
 RT "Prediction of the coding sequences of unidentified human genes. IX.  
 RT The complete sequences of 100 new cDNA clones from brain which can  
 RT code for large proteins in vitro.";  
 RL DNA Res. 5:31-39(1998).  
 RN [4]  
 RP SEQUENCE OF 4405-4439 FROM N.A.  
 RC TISSUE=Placenta;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,  
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length  
 RT human and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [5]  
 RP SEQUENCE OF 4405-5147 FROM N.A.  
 RA Kalicki J., Elliott G.;  
 RL Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.  
 CC -!- FUNCTION: May act as a scaffolding protein involved in the  
 CC organization of synaptic active zones and in synaptic vesicle  
 CC trafficking (By similarity).  
 CC -!- SUBUNIT: Interacts with Rabac1/Pral, RIMS2 and profilin (By  
 CC similarity).  
 CC -!- SUBCELLULAR LOCATION: Concentrated at the presynaptic side of  
 CC synaptic junctions (By similarity).  
 CC -!- ALTERNATIVE PRODUCTS:

```

CC      Event=Alternative splicing; Named isoforms=2;
CC      Comment=Additional isoforms seem to exist;
CC      Name=1;
CC      IsoId=Q9Y6V0-1; Sequence=Displayed;
CC      Name=2;
CC      IsoId=Q9Y6V0-2; Sequence=VSP_003923, VSP_003924, VSP_003925,
CC      VSP_003926, VSP_003927;
CC      Note=No experimental confirmation available;
CC      !- DOMAIN: C2 domain 1 is involved in binding calcium and
CC      phospholipids. Calcium binds with low affinity but with high
CC      specificity and induces a large conformational change.
CC      !- SIMILARITY: Contains 2 C2 domains.
CC      !- SIMILARITY: Contains 1 PDZ/DHR domain.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; Y19188; CAB60727.1; -.
DR      EMBL; AC004903; AAD20936.1; -.
DR      EMBL; AC004886; AAD21789.1; -.
DR      EMBL; AB011131; BAA25485.1; -.
DR      EMBL; BC001304; AAH01304.1; -.
DR      EMBL; AC004082; AAB97937.1; -.
DR      PIR; T00634; T00634.
DR      HSSP; P04410; 1A25.
DR      Genew; HGNC:13406; PCLO.
DR      MIM; 604918; -.
DR      GO; GO:0005856; C:cytoskeleton; NAS.
DR      GO; GO:0045202; C:synaptic junction; ISS.
DR      GO; GO:0005509; F:calcium ion binding; ISS.
DR      GO; GO:0005544; F:calcium-dependent phospholipid binding; ISS.
DR      GO; GO:0005522; F:profilin binding; ISS.
DR      GO; GO:0007010; P:cytoskeleton organization and biogenesis; ISS.
DR      GO; GO:0016080; P:synaptic vesicle targeting; ISS.
DR      InterPro; IPR000008; C2.
DR      InterPro; IPR001565; Synaptotagmin.
DR      PRINTS; PR00360; C2DOMAIN.
DR      PRINTS; PR00399; SYNAPTOTAGMN.
DR      SMART; SM00239; C2; 2.
DR      PROSITE; PS00499; C2_DOMAIN_1; 1.
DR      PROSITE; PS50004; C2_DOMAIN_2; 2.
KW      Calcium/phospholipid-binding; Zinc; Metal-binding; Zinc-finger;
KW      Repeat; Alternative splicing.
FT      NON_TER      1      1
FT      DOMAIN      400      465      10 X 10 AA TANDEM APPROXIMATE REPEATS OF
FT      P-A-K-P-Q-P-Q-Q-P-X.
FT      ZN_FING      499      523      C4-TYPE (POTENTIAL).
FT      ZN_FING      969      992      C4-TYPE (POTENTIAL).
FT      NON_CONS      1010      1011
FT      DOMAIN      2300      2325      POLY-PRO.
FT      DOMAIN      4391      4442      PDZ.
FT      DOMAIN      4544      4633      C2 DOMAIN 1.

```

FT	DOMAIN	5031	5121	C2 DOMAIN 2.
FT	VARSPLIC	4404	4404	S -> SGNGLGIRIVGGKEIPGHSGEIGAYIAKILPGGSAE
FT				QTGKLMEG (in isoform 2).
FT				/FTId=VSP_003923.
FT	VARSPLIC	4534	4534	K -> KPTDGTKVVSHPITGEIQ (in isoform 2).
FT				/FTId=VSP_003924.
FT	VARSPLIC	4576	4576	G -> GQVMVVQNAS (in isoform 2).
FT				/FTId=VSP_003925.
FT	VARSPLIC	4757	4761	TAHKS -> SKRRK (in isoform 2).
FT				/FTId=VSP_003926.
FT	VARSPLIC	4762	5147	Missing (in isoform 2).
FT				/FTId=VSP_003927.
SQ	SEQUENCE	5147 AA;	563537 MW;	CD5D84990498CD3C CRC64;

Query Match 5.4%; Score 320; DB 1; Length 5147;  
 Best Local Similarity 21.8%; Pred. No. 0.00015;  
 Matches 260; Conservative 152; Mismatches 440; Indels 340; Gaps 61;

Qy	8	PLVSSSDSPRPQPAFKYQFVREPEDEEEEEEEEEDEDEDLEELEVLERKPAAGLSAAP	67
		:        :    :	
Db	260	PSLPSPSKPPIQQPTPGKPPAQPGHEKSQPG-----PAKPPAQPSGLT	303
Qy	68	VPTAPAAGA---PLMDFGNDFVPPAPRGPLPAAPPV-----	100
		:	
Db	304	KPLAQQPGTVKPPVQPPGTTKPPAQPLG--PAKPPAQQTGSEKPSSEQPGPKALAQPPGV	361
Qy	101	--APERQPSWDPSVSTVPAPSPLS-----AAVSPSKLPEDDEPPA-----RPP	144
		:     :      :       :    :   :	
Db	362	GKTPAQQPG-PAKPPTQQVGTGPKPLAQQPGQLQSPAKAPGPTKTPAQTKPPSQPGSTKPP	420
Qy	145	P--PPPASVSPQAEPVWTPPAPAP-AAPPSTPAAPKRRGSSGAVVXXXXKIMDLKEQPGN	201
		:   :     :	
Db	421	PQQPGPAKPSPPQPGSTKPPSQPGSAKPSA-----QQPSP	456
Qy	202	TISAGQEDFPSVLLETAASXPSLSPLSAASFKEHEYLGNLSTVLPTEGTLQENVSEASKE	261
		:   :   : :      :     :     :	
Db	457	AKPSAQQ-FTKPVSTGFGKPLQPPTVSPSAKQPPSQGLPKTICPL-----CNTTELLH	510
Qy	262	VSEKA-----KTLII-----DRDLTEFSE-----LEYSEMGSFSVSPKA-----	296
		:   : :        :   :	
Db	511	VPEKANFNTCTECQTTVCSLCGFNPNPHLTEAKEWLCLNCQMKRALGGDLAPVPSSPQPK	570
Qy	297	-----ESAVIVANPREEIIIVKNKDEEEKLVSNILHXQQEL-----PTALTCLVKED	343
		:   :         :       :	
Db	571	LKTAPVTTTSAVSKSSPQQQTSPKKDAAPK-----QDLSKAPEPKPPPLVKQP	620
Qy	344	EVVSSEKAK-----DSFNEKRVAVEAPMREE-----YADFKPFERVWEVKDSKEDSDM	391
		:         : :   :        :   :	
Db	621	TLHGSPSAKAKQPPEADSLSKPAPPKEPSVQSEQDKAPVADDKP-----KQPKMVKPTTDL	676
Qy	392	LAAGGKIESNLESKVD---KKCFADSLEQTNHEKDSSESNDDTSFSPSTPEGIKDRSGAYI	448
		:::   : :      : :   : :       :	
Db	677	VSS-----SSATTKPDIPSSKVSQAEEKTTPPLKTDKAPVADDKP-----QKKEEPKKAQTKMSPK	723
Qy	449	TCAPFN-----PAATESIATNIFPLLE-----DPTSENXTDEKKIEEKKQIVTEKN	495
		:    :   : :       :	
Db	724	--TPFDSKAIPRPASDSKIISHPGPSSSESKGQKQVDPV-----QKKEEPKKAQTKMSPK	775

Qy 496 TSTK-----TSNPFFVAAQDSETDYVTTD-----NLTKVTEEVVANMPEGLT 537  
 | | | | : | | : | : |  
 Db 776 PDAKPMKGSPTPPGPRPTAGQTVPTPQQSPKPEQSRFSLNLSITD---APKSQPTT 832  
 Qy 538 PDLVQEACESELNEVTGKTIAYETKMDLVQTSSEVMQESLYPA--AQLCPSFEESEATPSP 595  
 | | | | : : | | : : | : | : | : |  
 Db 833 P---QET-----VTGKLFQFGASI-FSQASNLISTAGQPGPHSQSGPGAPMKQA-PAP 880  
 Qy 596 VLPDIVMEAPLNSA-VPSAGASVI-----QPSSSPLEASSVNYESIK--HEPENPPPY 645  
 | | : | | | | : | | : : | : | |  
 Db 881 SQPPTSQGPPKSTGQAPPAPAKSIPVKKETKAPAAEKLEPKAEQAPTVMKRTETETKPPPI 940  
 Qy 646 EEAMSVSLKVSGIKEEIKEPENINAALQETEAPYISACDLIK-ETKLSAEPAPDFSDYS 704  
 : : | : | : | : : | | | : : | : : | :  
 Db 941 KDSKSLT-----AEPQKAVLPTKLEKSPKPESTCPLCKTELNIGSKDPPNFNTCT 990  
 Qy 705 EMAKVE-----QPVPDHSELVE-----DSSPDSEPVDLFSDDS--- 737  
 | | : | : | | : | : : : |  
 Db 991 ECKNQVCNLCGFNPTPHLTENCQTQRAISQGLDIRKMPPAPSGPKASPMFVPTESSSQK 1050  
 Qy 738 --IPDVPQ-----KQD-----ETVML--VKESLTETSFESMIEYENKEKLSALPPEGG 781  
 : | | | : | : | | : | : | : | : | :  
 Db 1051 TAVP--PQVKLVKKQEVEVKTEAEKVILEKVETLSMEKIIPMVTTDQKQEESSKLEKDKA 1108  
 Qy 782 KPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFIKSEAQIRET 841  
 | | | | : : | : : | | | : | : | : | :  
 Db 1109 SALQE--KKPLPEEK-KLIPEE-EKIRSEEKKPLLEKKKPTP---EDKKLLPEAKTSAP 1160  
 Qy 842 ETFSD---SSPIEIIIDE-FPTLISSKTDSFSLKAREYTDLEVSHKSEIANAPDGA-GSLP 896  
 | | : | : | : | | | : : | | | |  
 Db 1161 EEQKHDLLKSQVQIAEEKLEGRVAPKTVQEGK-----QPQTKMEGLPSGTPQSLP 1210  
 Qy 897 CTELPDLSLKNI----QPKVEEKISFSDDFSNGSATSQVLLLPDVSALGHTQ----- 947  
 : | : | | | | : | : : | : | : | : :  
 Db 1211 KED---DKTTKTIKEQPQPCTAKPDQEKEDDKSDTSSSQPKSPQGLSDTGYSSDGISS 1267  
 Qy 948 --AEIESIVKPKVLEKEAEKKLPSDTEKEDRSPSAIFSADLGK--TSVVDLL 995  
 | | : : | : | | : : | : | : | : | : | :  
 Db 1268 SLGEIPSLIPTD--EKDILKGLKKDSFSQESSPSS--PSDLAKLESTVLSIL 1315

# RESULT 12

## PCLO\_MOUSE

ID PCLO\_MOUSE STANDARD; PRT; 5038 AA.  
 AC Q9QYX7; Q9QYX6; Q9QZJ0;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 10-OCT-2003 (Rel. 42, Last annotation update)  
 DE Piccolo protein (Presynaptic cytomatrix protein) (Aczonin) (Brain-derived HLMN protein).  
 GN PCLO OR ACZ.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]

RP SEQUENCE FROM N.A., SUBCELLULAR LOCATION, ALTERNATIVE SPLICING,  
RP TISSUE SPECIFICITY, AND INTERACTION WITH PROFILIN.  
RC TISSUE=Brain;  
RX MEDLINE=99439764; PubMed=10508862;  
RA Wang X., Kibschull M., Laue M.M., Lichte B., Petrasch-Parwez E.,  
RA Kilimann M.W.;  
RT "Aczonin, a 550-kd putative scaffolding protein of presynaptic active  
RT zones, shares homology regions with rim and bassoon and binds  
RT profilin.";  
RL J. Cell Biol. 147:151-162(1999).

RN [2]

RP REVISIONS.

RA Kilimann M.W.;

RL Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

RN [3]

RP SEQUENCE OF 4502-4682 FROM N.A.

RC TISSUE=Brain;

RA Huang W., Jin W., Huang C., Chen B., Zhang J., Ju G.;

RL Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

RN [4]

RP INTERACTION WITH RIMS2.

RX MEDLINE=22384373; PubMed=12401793;

RA Fujimoto K., Shibasaki T., Yokoi N., Kashima Y., Matsumoto M.,

RA Sasaki T., Tajima N., Iwanaga T., Seino S.;

RT "Piccolo, a Ca<sup>2+</sup> sensor in pancreatic beta-cells. Involvement of

RT cAMP-GEFII.Rim2.Piccolo complex in cAMP-dependent exocytosis.";

RL J. Biol. Chem. 277:50497-50502(2002).

CC -!- FUNCTION: May act as a scaffolding protein involved in the  
CC organization of synaptic active zones and in synaptic vesicle  
CC trafficking.

CC -!- SUBUNIT: Interacts with Rabac1/Pral, RIMS2 and profilin.

CC -!- SUBCELLULAR LOCATION: Concentrated at the presynaptic side of  
CC synaptic junctions.

CC -!- ALTERNATIVE PRODUCTS:

CC Event=Alternative splicing; Named isoforms=2;

CC Name=1;

CC IsoId=Q9QYX7-1; Sequence=Displayed;

CC Name=2;

CC IsoId=Q9QYX7-2; Sequence=VSP\_003928, VSP\_003929;

CC -!- TISSUE SPECIFICITY: Highly expressed in brain. Low levels found in  
CC stomach. Not detected in other tissues analyzed including adrenal  
CC gland, testis and pancreas.

CC -!- DOMAIN: C2 domain 1 is involved in binding calcium and  
CC phospholipids. Calcium binds with low affinity but with high  
CC specificity and induces a large conformational change.

CC -!- SIMILARITY: Contains 2 C2 domains.

CC -!- SIMILARITY: Contains 1 PDZ/DHR domain.

CC -----  
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CC -----

DR EMBL; Y19185; CAB60731.2; -.



DR EMBL; Y19186; CAB60732.2; -.  
 DR EMBL; AF181269; AAD55786.2; -.  
 DR HSSP; P04410; 1A25.  
 DR MGD; MGI:1349390; Pclo.  
 DR GO; GO:0045202; C:synaptic junction; IDA.  
 DR GO; GO:0005509; F:calcium ion binding; ISS.  
 DR GO; GO:0005544; F:calcium-dependent phospholipid binding; ISS.  
 DR GO; GO:0005522; F:profilin binding; IDA.  
 DR GO; GO:0019933; P:cAMP-mediated signaling; IDA.  
 DR GO; GO:0007010; P:cytoskeleton organization and biogenesis; IDA.  
 DR GO; GO:0030073; P:insulin secretion; IDA.  
 DR GO; GO:0017157; P:regulation of exocytosis; IDA.  
 DR GO; GO:0016080; P:synaptic vesicle targeting; NAS.  
 DR InterPro; IPR000008; C2.  
 DR InterPro; IPR001478; PDZ.  
 DR InterPro; IPR008899; Znf\_piccolo.  
 DR Pfam; PF00168; C2; 2.  
 DR Pfam; PF00595; PDZ; 1.  
 DR Pfam; PF05715; Zf\_piccolo; 2.  
 DR SMART; SM00239; C2; 2.  
 DR SMART; SM00228; PDZ; 1.  
 DR PROSITE; PS00499; C2\_DOMAIN\_1; 1.  
 DR PROSITE; PS50004; C2\_DOMAIN\_2; 2.  
 DR PROSITE; PS50106; PDZ; 1.  
 KW Calcium/phospholipid-binding; Metal-binding; Zinc; Zinc-finger;  
 KW Repeat; Alternative splicing.  
 FT DOMAIN 371 470 10 X 10 AA TANDEM APPROXIMATE REPEATS OF  
 FT P-A-K-P-Q-P-Q-Q-P-X.  
 FT ZN\_FING 502 526 C4-TYPE (POTENTIAL).  
 FT ZN\_FING 967 990 C4-TYPE (POTENTIAL).  
 FT DOMAIN 2305 2329 POLY-PRO.  
 FT DOMAIN 4394 4488 PDZ.  
 FT DOMAIN 4607 4705 C2 DOMAIN 1.  
 FT DOMAIN 4922 5012 C2 DOMAIN 2.  
 FT VARSPLIC 4829 4833 TKPTN -> SKRRK (in isoform 2).  
 FT /FTId=VSP\_003928.  
 FT VARSPLIC 4834 5038 Missing (in isoform 2).  
 FT /FTId=VSP\_003929.  
 SQ SEQUENCE 5038 AA; 547600 MW; DADA460CF3B40888 CRC64;

Query Match 5.3%; Score 315; DB 1; Length 5038;  
 Best Local Similarity 22.0%; Pred. No. 0.00023;  
 Matches 254; Conservative 136; Mismatches 435; Indels 328; Gaps 57;

Qy 57 RKPA--AGLSAAPVPTAPAAGAPLMDFG---NDFVPPAPR-----GPLPAAPPVAPE 103  
 : || || : | | | | : | : | : |  
 Db 288 KSPAQPA GTGKSPAQPPVTAKPPAQQAGLEKTSLQQPGPKSLAQTPGQGVPPGPAKSPA 347  
 Qy 104 RQ-----PSWDPSP-VSSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQ-A 155  
 : | : | | : | | | : | | | | : | | | |  
 Db 348 QQPGTAKLPAQQPGPQTASKVPGPTKTPAQLSGPGKTPAQQPGPTKPSPPQPIPAKPQPQ 407  
 Qy 156 EPVWT---PPAPAPAAPP---STPAAPKRRGSSGAVVXXXXKIMDLKEQPGNTISAGQED 209  
 : || | | || | | || | : : : | | | | :  
 Db 408 QPVATKPQPQPAPAKPQPQHPTPAKPQPQOPTPA-----KPQPQOPTPAKPQP 456  
 Qy 210 FPSVLLETAASXPSLS-----PLSA--ASFKEHEYLGNLSTVLP---TEGTLQENV 256

Db	457 QHPGLGKPSAQQPSKSI	516
Qy	257 EASKEVSEKAKTLLI-----DRDLTEFSEL-----EYSEMGSSFSVSPKA	296
Db	517 KANFNTCTECQSTVCSL	576
Qy	297 ESAVIV-----ANPREEIIVKN---KDEEEK---LVSNNILHX-----QQE	331
Db	577 ASVQPATASKSPVPSQQASPKKELPSKQDSPKAPESKKPPPLVKQPTLHGPTPATAPQPP	636
Qy	332 LPTALTCLV--KEDEVVSSEKAKDSFNEKRVAVEAPMREEYADFKPFERVWEVKDSKEDS	389
Db	637 VAEALPKPAPPKKPSAALPEQAK-----APV---ADVEPKQP--KTTETLTDS	679
Qy	390 DMLAAGGKIESNLESKVDKCFADSLEQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYIT	449
Db	680 PSSAAATSKPAILSSQVQ---AQAQVTTAPPLKTDSAKTSQSFPTGD-----T	725
Qy	450 CAPFN-----PAATESIATNIFPLLEDPTSSENXTD-EKKIEEKKAQIVTEKNTSTKTSN	502
Db	726 ITPLDSKAMPRPASDSKIVSH-----PGPTSESKDPVQKKEEPKKAQTKVTPKPDTK---	777
Qy	503 PFFVAAQDSETDYVTTDNLT	546
Db	778 PVPKGSPTPSGTRPTTGQATPQSQQPPKPPEQSRFSLNLGGIADAPKS-QPTTPQET--	834
Qy	547 SELNEVTGTKIAYETKMDLVQTSEVMQESLYPAAQLCPSFEESEATPSPVLP----	602
Db	835 -----VTGKLFGFGASI-FSQASNLIS---TAGQQAPHPQTGPAAPSKQAPPPSQT	884
Qy	603 EAPLNSA--VPSAGASVIQ-----PSSSPLEASSVNYESI-----KHEP---ENPP	643
Db	885 QGPPKSTGQHPSAPAKTTAVKKETKGPAENLEAKPAQAPT	944
Qy	644 PYEEAMSVSLKVSGIKEEIKEPENINAALQETEAPYISIACDLIK-ETKLSAEPAPDFSD	702
Db	945 P-----TEPEKAVLAQKPDKTTKPKPACPLCRTELNVGSQDPPNFNT	986
Qy	703 YSEMAKVE-----QPVPDHSELVE-----DSSPDSEPVD	731
Db	987 CTECKNQVCNLGCFNPTPHLTEIQEWLCLNCQ	1046
Qy	732 LFSD-----DSIPDVPQKQDETV-----MLVKESLT	757
Db	1047 APAEPPPQKTPTAAHAKGKKKETE	1106
Qy	758 ETSFESMIEYENKEKLSAL-----PPEGKPYLESFKLSLDNTKDTLLPDEVSTLSK	809
Db	1107 KSLVSVLPEKKPSEEEKALPADKKEKKPPAAEAPPLEEKKPI	1164
Qy	810 KEKIPLQMEELSTAVYSNDDL	868
Db	1165 GEE---KRDLLKAHVQIPEEGPIGKVASLACEGEQQPDTRPEDLPGATPQTLPKD-----	1216
Qy	869 KLAREYTDLEVSHKSEIANAPDGAG--SLPCTELPHDLS--LKNIQPKVEEKISFSDDFS	924

Db 1217 ---RQKESRDVTQPQAEGTAKEGRGEPSKDRTEKEEDKSDTSSSQPKSPQGLS-DTGYS 1272

Qy 925 KNGSATSKVLLLPDVSALGHTQAEIESIVKPKVLEKEAEKKLPDTEKEDRSPSAIFSA 984  
 :| : | || || |:: ||: || | : :| | : :  
 Db 1273 SDGISGS-----LG---EIPSLIPSD--EKDLLKGLKKDSFSQESSPSS--PS 1313

Qy 985 DLGK--TSVVDLL 995  
 || | :| :|  
 Db 1314 DLAKLESTVLSIL 1326

RESULT 13

ANK2\_HUMAN

ID ANK2\_HUMAN STANDARD; PRT; 3924 AA.  
 AC Q01484; Q01485;  
 DT 01-APR-1993 (Rel. 25, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 28-FEB-2003 (Rel. 41, Last annotation update)  
 DE Ankyrin 2 (Brain ankyrin) (Ankyrin B) (Ankyrin, nonerythroid).  
 GN ANK2.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).  
 RC TISSUE=Brain stem;  
 RX MEDLINE=91302466; PubMed=1830053;  
 RA Otto E., Kunimoto M., McLaughlin T., Bennett V.;  
 RT "Isolation and characterization of cDNAs encoding human brain  
 RT ankyrins reveal a family of alternatively spliced genes.";  
 RL J. Cell Biol. 114:241-253(1991).  
 RN [2]  
 RP REVISIONS.  
 RA Carpenter S.;  
 RL Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Brain stem;  
 RX MEDLINE=94075409; PubMed=8253844;  
 RA Chan W., Kordeli E., Bennett V.;  
 RT "440-kD ankyrinB: structure of the major developmentally regulated  
 RT domain and selective localization in unmyelinated axons.";  
 RL J. Cell Biol. 123:1463-1473(1993).  
 RN [4]  
 RP SEQUENCE OF 463-495 FROM N.A.  
 RX MEDLINE=92009921; PubMed=1833308;  
 RA Tse W.T., Menninger J.C., Yang-Feng T.L., Francke U., Sahr K.E.,  
 RA Lux S.E., Ward D.C., Forget B.G.;  
 RT "Isolation and chromosomal localization of a novel nonerythroid  
 RT ankyrin gene.";  
 RL Genomics 10:858-866(1991).  
 CC -!- FUNCTION: Attach integral membrane proteins to cytoskeletal  
 CC elements. Also bind to cytoskeletal proteins.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=3;  
 CC Name=1;

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CC      IsoId=Q01484-1; Sequence=Displayed;
CC      Name=2;
CC      IsoId=Q01484-2; Sequence=VSP_000267, VSP_000268;
CC      Name=3;
CC      IsoId=Q01484-3; Sequence=VSP_000268;
CC      -!- TISSUE SPECIFICITY: Plasma membrane of neurons as well as glial
CC          cells throughout the brain.
CC      -!- PTM: Phosphorylated at multiple sites by different protein kinases
CC          and each phosphorylation event regulates the protein's structure
CC          and function (Potential).
CC      -!- SIMILARITY: Contains 23 ANK repeats.
CC      -!- SIMILARITY: Contains 1 death domain.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; X56957; CAA40278.1; -.
DR      EMBL; X56958; CAA40279.2; -.
DR      EMBL; Z26634; CAB42644.1; -.
DR      EMBL; M37123; AAA62828.1; -.
DR      PIR; S37431; S37431.
DR      HSSP; P42771; 1DC2.
DR      Genew; HGNC:493; ANK2.
DR      MIM; 106410; -.
DR      InterPro; IPR002110; ANK.
DR      InterPro; IPR000488; Death.
DR      InterPro; IPR000906; ZU5.
DR      Pfam; PF00023; ank; 24.
DR      Pfam; PF00531; death; 1.
DR      Pfam; PF00791; ZU5; 1.
DR      PRINTS; PR01415; ANKYRIN.
DR      SMART; SM00248; ANK; 22.
DR      SMART; SM00005; DEATH; 1.
DR      SMART; SM00218; ZU5; 1.
DR      PROSITE; PS50088; ANK_REPEAT; 20.
DR      PROSITE; PS50297; ANK_REP_REGION; 1.
DR      PROSITE; PS50017; DEATH_DOMAIN; 1.
KW      Cytoskeleton; Alternative splicing; Repeat; ANK repeat;
KW      Phosphorylation.
FT      REPEAT      63      92      ANK 1.
FT      REPEAT      96      125     ANK 2.
FT      REPEAT     129      158     ANK 3.
FT      REPEAT     162      191     ANK 4.
FT      REPEAT     193      220     ANK 5.
FT      REPEAT     232      261     ANK 6.
FT      REPEAT     265      294     ANK 7.
FT      REPEAT     298      327     ANK 8.
FT      REPEAT     331      360     ANK 9.
FT      REPEAT     364      393     ANK 10.
FT      REPEAT     397      426     ANK 11.
FT      REPEAT     430      459     ANK 12.
FT      REPEAT     463      492     ANK 13.

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FT	REPEAT	496	525	ANK 14.
FT	REPEAT	529	558	ANK 15.
FT	REPEAT	562	591	ANK 16.
FT	REPEAT	595	624	ANK 17.
FT	REPEAT	628	657	ANK 18.
FT	REPEAT	661	690	ANK 19.
FT	REPEAT	694	723	ANK 20.
FT	REPEAT	727	756	ANK 21.
FT	REPEAT	760	789	ANK 22.
FT	REPEAT	793	822	ANK 23.
FT	DOMAIN	1773	1950	REPEAT-RICH REGION.
FT	REPEAT	1773	1784	REPEAT A.
FT	REPEAT	1785	1796	REPEAT A.
FT	REPEAT	1797	1808	REPEAT A.
FT	REPEAT	1809	1820	REPEAT A.
FT	REPEAT	1821	1832	REPEAT A.
FT	REPEAT	1833	1844	REPEAT A.
FT	REPEAT	1845	1856	REPEAT A.
FT	REPEAT	1857	1867	REPEAT A (APPROXIMATE).
FT	REPEAT	1868	1879	REPEAT A.
FT	REPEAT	1880	1891	REPEAT A.
FT	REPEAT	1892	1902	REPEAT A (APPROXIMATE).
FT	REPEAT	1903	1914	REPEAT A.
FT	REPEAT	1915	1926	REPEAT A.
FT	REPEAT	1927	1938	REPEAT A.
FT	REPEAT	1939	1950	REPEAT A.
FT	DOMAIN	3536	3620	DEATH.
FT	VARSPLIC	1039	1039	Q -> QFLGKLHLPTAPPPLNEGESLVSRILQLGPPGTK
FT				(in isoform 2).
FT				/FTid=VSP_000267.
FT	VARSPLIC	1444	3528	Missing (in isoform 2 and isoform 3).
FT				/FTid=VSP_000268.
FT	CONFLICT	475	476	GQ -> PE (IN REF. 4).
FT	CONFLICT	971	971	I -> S (IN REF. 1).
FT	CONFLICT	3581	3582	QY -> HA (IN REF. 1).
FT	CONFLICT	3586	3586	I -> Y (IN REF. 1).
SQ	SEQUENCE	3924	AA; 430337	MW; 52AC496C428E29D2 CRC64;

Query Match 5.0%; Score 299; DB 1; Length 3924;  
 Best Local Similarity 21.5%; Pred. No. 0.00069;  
 Matches 258; Conservative 167; Mismatches 417; Indels 358; Gaps 62;

Qy	14	DSPP-----RPQPAFKYQFVREPEDEEEEEEEEEDEDEDLE-----ELEVLERK	58
		:    : :::::    :	
Db	1648	DIPDETQSTQKQHKPSLGIKKPVRRKLKEKQKQKEEGLQASAEKAEKKGSSSEESLGED	1707
Qy	59	PAAGLSAAPVPTAPAAGAPLMD-----FGNDFVPPAPRG----	92
		:  :    : ::   :  :	
Db	1708	P--GLAPEPLPTVKAT-SPLIETPIGSIKDKVKALQKRVEDEQKGRSKLPPIRVKGKEDV	1764
Qy	93	-----PLPAA-PPVAPERQPSWDPS-----VSSTVPAPSPL	123
		:	
Db	1765	PKKTTHRHPAASPSLKSERHAPGSPSPKTERHSTLSSSAKTERHPPVSPSSKTEKHSPV	1824
Qy	124	SAAA-----VSPSKLPEDDEPPA-----RPPPPPPASVSPQAEPVW	159
		:          :       : : :	
Db	1825	SPSAKTERHSPASSSSKTEKHSPVSPSTKTERHSPVSSTKTERHPPVSPSGKTDKRPPV-	1883

Qy	160	TPAPAPAAPSTPAAPKRR---GSSGAVVXXXXKIMDLKEQPGNTISAGQEDFPSVLLE	216
Db	1884	SPSGRTEKHPPVSPGRTEKRLPVSPSGRTD-----KHQPVSTAGKTEKHLPVSPSG	1934
Qy	217	TAASXPSLSPLSAAS-FKEHEYLGNLSTVLPT-----EGTLQENVSEASKEVSEKAKT	268
Db	1935	KTEKQPPVSPTSSTERIEETMSVRELKMAFQSQGDPSKHKTGLFEHKSAAKQKQPQEKGV	1994
Qy	269	-----LLIDRDLTEFSELEYSEMSSFSVSPKAES--AVIVANPREEIIIVKNKDE--	316
Db	1995	RVEKEKGPILTQRE-AQKTENQTIKRGQRLPVTGTAESKRGVRVSS----IGVKKEDAAG	2049
Qy	317	-EEKLVSNNI-----LHXQQELPTALTCLVKE-----DEVV	346
Db	2050	GKEKVLSHKIPEPVQSVPEEESHRESEVPK--EKMADEQGMDLQISPDRKTSTDFSEVI	2107
Qy	347	SSE-KAKDSFNEKRVAVEAPMREEYAD---FKPFERVWEVKDSKED-----	388
Db	2108	KQLEDNDKYQQFRLSEETEKALHLDDQVLTSPFNTTFPLDYMKDEFLPALSLQSGALDG	2167
Qy	389	-SDMLAAGGKIESNLESKVDKKCFADSLEQTNHE--KDSESSNDDTSFPSTPEGIKDRS	444
Db	2168	SSESLKNEGVAGSPCGSLMEGTPQISSEESYKHEGLAETPETSPELSF--SPKKSEEQT	2225
Qy	445	GAYITCAPFNPAATESIATNIFPLLEDPTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPF	504
Db	2226	G-----ETKESTKTETTTEIRSEKEHPTTKDITGGS--EERGATVTEDSETSTESFQKE	2277
Qy	505	FVAAQDSETDYVTTDNLTKVTEEVA-NMPEGLTPDLVQEACESELNEVTGTIAIYETKM	563
Db	2278	ATLGSPKDTSPKRQDDCTGSCSVALAKETPTGLT----EEAACDEGQRTFGSS-AHKT--	2330
Qy	564	DLVQTSEVMQESLYPAAQLCPSFEESEATPSPVL-----PDIVMEAP--LNSAV	610
Db	2331	---QTDSEAQES-----TATSDETKALPLPEASVKTDGTGTESKPQGVIRSPQGLELAL	2380
Qy	611	PSAGASVIQ-----PSSSPLEASSVNYESIKHE-PEN--PPPYEEA-MSVSLKVSG	657
Db	2381	PSRDSEVL SAVADDSLAVSHKDSLEASPVLEDNSSHKT PDSLEPSPLKESPCRDSLESSP	2440
Qy	658	IKEEIKE---PEN--INAALQETE--APYISIACDLIKETKLSAEPAPDFSDYSEMAKVE	710
Db	2441	VEPKMKAGIFPSHFPLPAAVAKTELLTEVASVRSRLLRD-----PDGS--AEDDSLE	2490
Qy	711	QVPDPHSELVEDS-----SPDSEPVDLFSDDSI PDVPQKQDETVMVLKESLTETSFESMI	765
Db	2491	Q-----TSLMESSGKSPLSPDTPSSEEVS YEVT PKTTDVSTPKPAVIHECAEED-----	2539
Qy	766	EYENKEKLSALPPEGGKPYLESFKLSLDNTKDTLLPDEVSTLSKK---EKIPLQMEELS	821
Db	2540	DSENGEKKRFTPEE-----EMFKMV---TKIKMF-DELEQEAQKRDYKKEPKQEES	2589
Qy	822	TAVYSNDDLFI SKEA-QIRETETFS DSSPIEII DEFPTLISSKTD SFSKLAREYTDLEVS	880
Db	2590	S---SDPDADCSVDVDEPKHTGSGEDES GV-----PVLVTSES RKVSSSSSES-----	2633

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QY      881 HKSEIANAPDGAGS-----LPCTELPHDLSLKN-----IQPKVEEKISF--SDD 922
      : |:|   || |   | : || :   :   || | :: :| :|
Db      2634 -EPELAQLKKGADSGLLPEPVIRVQPPSPLPSSMDSNSSPEEVQFQPVVSKQYTFKMNE 2692

QY      923 FSKNGSATSKVLLLLPPDVSA LGHTQAEIESIVKPKVLEKEAEKKLPD-----TEKEDRS 977
      :   : :   ||::| | |   || |||
Db      2693 TQEEP GKSEE-----EKDSESHLAEDRHAVSTEAEDRS 2725

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RESULT 14

MAPB\_HUMAN

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ID      MAPB_HUMAN      STANDARD;      PRT; 2468 AA.
AC      P46821;
DT      01-NOV-1995 (Rel. 32, Created)
DT      01-NOV-1995 (Rel. 32, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Microtubule-associated protein 1B (MAP 1B) [Contains: MAP1 light chain
DE      LC1].
GN      MAP1B.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Fetal brain;
RX      MEDLINE=95104835; PubMed=7806212;
RA      Lien L.L., Feener C., Fischbach N., Kunkel L.M.;
RT      "Cloning of human microtubule-associated protein 1B and the
RT      identification of a related gene on chromosome 15.";
RL      Genomics 22:273-280(1994).
CC      -!- FUNCTION: The function of brain MAPS is essentially unknown.
CC      Phosphorylated MAP1B may play a role in the cytoskeletal changes
CC      that accompany neurite extension. Possibly MAP1B Binds to at least
CC      two tubulin subunits in the polymer, and this bridging of subunits
CC      might be involved in nucleating microtubule polymerization and in
CC      stabilizing microtubules.
CC      -!- SUBUNIT: 3 different light chains, LC1, LC2 and LC3, can associate
CC      with MAP1A and MAP1B proteins.
CC      -!- DOMAIN: Has a highly basic region with many copies of the sequence
CC      KKEE and KKEI/V, repeated but not at fixed intervals, which is
CC      responsible for the binding of MAP1B to microtubules.
CC      -!- PTM: LC1 is coexpressed with MAP1B. It is a polypeptide generated
CC      from MAP1B by proteolytic processing. It is free to associate with
CC      both MAP1A and MAP1B. It interacts with the amino-terminal region
CC      of MAP1B (By similarity).
CC      -!- SIMILARITY: TO MAP1A.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
CC      use by non-profit institutions as long as its content is in no way
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL; L06237; AAA18904.1; -.

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DR Genew; HGNC:6836; MAP1B.  
 DR MIM; 157129; -.  
 DR GO; GO:0005875; C:microtubule associated complex; TAS.  
 DR InterPro; IPR000102; MAP1B\_neuraxin.  
 DR Pfam; PF00414; MAP1B\_neuraxin; 10.  
 DR PROSITE; PS00230; MAP1B\_NEURAXIN; 6.  
 KW Microtubule; Repeat; Phosphorylation.  
 FT CHAIN ? 2468 MAP1 LIGHT CHAIN LC1.  
 FT REPEAT 1878 1894 MAP1B 1.  
 FT REPEAT 1895 1911 MAP1B 2.  
 FT REPEAT 1912 1928 MAP1B 3.  
 FT REPEAT 1929 1945 MAP1B 4.  
 FT REPEAT 1946 1962 MAP1B 5.  
 FT REPEAT 1963 1979 MAP1B 6.  
 FT REPEAT 1997 2013 MAP1B 7.  
 FT REPEAT 2014 2030 MAP1B 8.  
 FT REPEAT 2031 2047 MAP1B 9.  
 FT REPEAT 2048 2064 MAP1B 10.  
 FT DOMAIN 589 790 LYS-RICH (HIGHLY BASIC, CONTAINS MANY  
 KKEE AND KKEI/V REPEATS).  
 SQ SEQUENCE 2468 AA; 270618 MW; 540839CBDF09D461 CRC64;

Query Match 5.0%; Score 296.5; DB 1; Length 2468;  
 Best Local Similarity 21.5%; Pred. No. 0.00049;  
 Matches 264; Conservative 148; Mismatches 459; Indels 355; Gaps 59;

QY 2 EDLDQSPLVSSS-DSPPRPQPAFKYQ---FVREP-----EDEE 35  
 || :: ||:| || : : | : ::|| | |:  
 Db 956 EDGEEHVCVSASKHSPTEDDEESAKAEADAYIREKRESVASGDDRAEEDMDEAIEKGEAEQ 1015  
 QY 36 EEEEEEEDEDEDLEEELEV-LERKPAAGLSAAPVPTAPAAGAPLMDFGNDFVPAPRGPL 94  
 :||| :|||: || | | | : | | | | : | | |  
 Db 1016 SEEEADEEDKAEDAREEEYEPEKMEAEDYVMVVDKAAEAGGAEEQYGLFTTPTKQLG-- 1073  
 QY 95 PAAPPVAPERQPSWDPSPVSVSTVPAPSPLSAAAVSPSKLPEDDEPPARPPPPPPASVSPQ 154  
 : | | : | | : | | | | : | | | | : | | :  
 Db 1074 ----AQSPGREPA--SSIHDETLPGGSESEATA-----SDEENREDQPEEFTATSGYT 1120  
 QY 155 AEPVWTPPAPAPAAPSTPAAPKRRGSSGAVVXXXXKIMDLKEQPGNTISAGQE----D 209  
 : | | | | | : | : | | | |  
 Db 1121 QSTIEISSEPTPMDEMSTP-----RDVMSDETNNETESPSQEFVNITK 1164  
 QY 210 FPSVLLETAASXPS-LSPLSAASFKE-----HEYLGNLSTVLPTEGTLQENVSEAS 259  
 : | | | | : : || : | | : | : || : | : : | : :  
 Db 1165 YESSLYSQEYSKPADVTPLN--GFSEGSKTDATDGKDYNASASTISPPSSMEEDKFSRSA 1222  
 QY 260 -----KEVSEKAKTLLIDRDLTEF-----SELEYSEMGS---SFS 291  
 | | | | | : | | | : | : | : | : | :  
 Db 1223 LRDAYCSEV--KASTTLDIKDSISAVSSEKVSPSKSPSLSPSPSPPLEKTPLGERSVNF 1280  
 QY 292 VSP-----KAESAVIVANPR--EEIIVKN--KDEEEKL-----VSNNILHX----- 328  
 : | | | | : | : | : | : | : | : | : | : | : | :  
 Db 1281 LTPNEIKVSAEAEVAPVSPEVTQEVVEEHCA SPEDKTLEVVSQSVTGSAGHTPPYQSP 1340  
 QY 329 ----QOELPTALTKLVKEDEVVSSEKAKDSFNEKRVAVEAPMREEYADFK-PFERVWEVK 383  
 | | | : : | | | : | : | : | : | : | : | : | :  
 Db 1341 TDEKSSHLPTEV--IEKPPAVPVSF EFSDAKDENERASVSPMDEPVPDSESPIEKVL SPL 1398



Qy 384 DSKEDSDMLAAGGKIESNLESKVDDKCFADSLEQTNHEKDSSESSNDDTSFPSTPEGIKDR 443  
 | : : | | : | | | : : | :  
 Db 1399 RS---PPLIGSESAYESFLSA--DDKASGRGAESPFEKSGKQGSPDQVSPVSE----- 1447

Qy 444 SGAYITCAPFNPAATESIATNIFPLLEDPTSENXTDEKK-----IEEKK-----A 488  
 : | | : : | : | | | : : : : :  
 Db 1448 ----MTSTSLYQDKQEGKSTDFAPIKEDFGQEKKTDDVEAMSSQPALALDERKLGDSVPT 1503

Qy 489 QI-----VTEKNTSTKTSNPFVAAQDSETDYVTTDNLTKVTEEVVA--N 531  
 | | : : | | : : | | : : | : | :  
 Db 1504 QIDVSQFGSFKEDTKMSISEGTVSDKSATP--VDEGVAEDTYSHMEGVASVSTASVATSS 1561

Qy 532 MPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQES-LYPAAQLCP----- 584  
 | | | : : : : : : : : : : : :  
 Db 1562 FPEPTTDD-VSPSLHAEVGSPhSTEVDDSLSVSVVQTPTTFQETEMSPSKEECPRPMSIS 1620

Qy 585 -----SFESEATPSPVLP-DIVMEAPLNSAVPSAGASVI 618  
 | | : : | | : : | : | :  
 Db 1621 PPDFSPKTAKSRTPVQDHRSEQSSMSIEFGQESPEQSLAMDFSRQSPDH---PTVGAGVL 1677

Qy 619 Q-----PSSSPLEASSVNYESIKHE--PENPPPY-----EEAMSVS-LKVSIGIKEEIKE 664  
 | : | : | : | | | : | : : :  
 Db 1678 HITENGPTEVDYSPSDMQDSSLSHKIPMEEPSYTDNDLSELISVSQVEASPSTSSAHT 1737

Qy 665 PENINAALQETE----AP-----YISIACDLIKE---TKLSAEP-----A 697  
 | | : | | | | : : : : | : : :  
 Db 1738 PSQIASPLQEDTLSDVAPPRDMSLYASLTSEKVQSLEGEKLSPKSDISPLTPRESSPLY 1797

Qy 698 PDFSDYSEMAKVEQVPDPHSELVEDSSPDSEPVDLFS----- 734  
 | | | : | : | | | | : | |  
 Db 1798 PTFSDSTSAVK-EKTATCHS----SSSP---PIDAASAEPYGFRAVLFDTMQHHLLALNR 1849

Qy 735 DDSIPDVP-----QKQDETVMVLVKESLTETSFESMIEYENKEKLSALPPE 779  
 | | | : | | : | | | : | : | :  
 Db 1850 DLSTPGLEKDSGGKTPGDFSYAYQKPEET-----TRSPDEEDYDYESYEKTTTRTSDV 1901

Qy 780 GGKPYLESFKLSLDNTKDTLLPDEVSTLSKKEKIPLQMEELSTAVYSNDDLFIKEAQIR 839  
 | | | : : : | : | : | | | : | :  
 Db 1902 GGY-YYEKIERTTKSPSDSGYSYE--TIGKTTKTP-----EDGDYSYE--IEKTTTRTP 1950

Qy 840 ETETFSDSPIEIIIDEFPTLISSKTDS---FSKLAREYTDLEVSHKSEIANAPDGAGSLP 896  
 | : | | | | | : | : : : | :  
 Db 1951 EEGGYSYD-----ISEKTTSPPEVSGYSYEKTERSRLLDISNGYDDS---- 1994

Qy 897 CTELPHDLSLKNIQPKVEEKISFSDDFSKNGSATSKVLLLPDVSALGHTQAE-IESIVK 955  
 : | | : : | : : | | | : | : :  
 Db 1995 -EDGGHTLGDPSYSYETTEKITSFPESEGYSETSTKTTTRTPDTSTYCYETAEKITRTPQ 2053

Qy 956 PKVLEKE-----AEKKLPDTEKE 974  
 | | | | : :  
 Db 2054 ASTYSYETSDLCYTAEEKSPSEARQD 2079

RESULT 15

MAPB\_RAT

ID MAPB\_RAT STANDARD; PRT; 2459 AA.

AC P15205; Q62958; Q9ER21; Q9QW92;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Microtubule-associated protein 1B (MAP 1B) (Neuraxin) [Contains: MAP1  
DE light chain LC1].  
GN MAP1B.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE OF 1-142 FROM N.A.  
RC STRAIN=Sprague-Dawley; TISSUE=Testis;  
RX MEDLINE=96257242; PubMed=8666295;  
RA Liu D., Fischer I.;  
RT "Isolation and sequencing of the 5' end of the rat microtubule-  
RT associated protein (MAP1B)-encoding cDNA.";  
RL Gene 172:307-308(1996).  
RN [2]  
RP SEQUENCE OF 96-2459 FROM N.A., DOMAIN, AND INDUCTION.  
RC STRAIN=Sprague-Dawley; TISSUE=Brain, and Glial tumor;  
RX MEDLINE=92347374; PubMed=1639092;  
RA Zauner W., Kratz J., Staunton J., Feick P., Wiche G.;  
RT "Identification of two distinct microtubule binding domains on  
RT recombinant rat MAP 1B.";  
RL Eur. J. Cell Biol. 57:66-74(1992).  
RN [3]  
RP SEQUENCE OF 1541-2459 FROM N.A., AND TISSUE SPECIFICITY.  
RC TISSUE=Spinal cord;  
RX MEDLINE=90059871; PubMed=2555150;  
RA Rienitz A., Grenningloh G., Hermans-Borgmeyer I., Kirsch J.,  
RA Littauer U.Z., Prior P., Gundelfinger E.D., Schmitt B., Betz H.;  
RT "Neuraxin, a novel putative structural protein of the rat central  
RT nervous system that is immunologically related to microtubule-  
RT associated protein 5.";  
RL EMBO J. 8:2879-2888(1989).  
RN [4]  
RP DEVELOPMENTAL STAGE, AND PHOSPHORYLATION.  
RX MEDLINE=97405699; PubMed=9260743;  
RA Ma D., Nothias F., Boyne L.J., Fischer I.;  
RT "Differential regulation of microtubule-associated protein 1B (MAP1B)  
RT in rat CNS and PNS during development.";  
RL J. Neurosci. Res. 49:319-332(1997).  
CC -!- FUNCTION: The function of brain MAPS is essentially unknown.  
CC Phosphorylated MAP1B may play a role in the cytoskeletal changes  
CC that accompany neurite extension. Possibly MAP1B Binds to at least  
CC two tubulin subunits in the polymer, and this bridging of subunits  
CC might be involved in nucleating microtubule polymerization and in  
CC stabilizing microtubules.  
CC -!- SUBUNIT: 3 different light chains, LC1, LC2 and LC3, can associate  
CC with MAP1A and MAP1B proteins.  
CC -!- TISSUE SPECIFICITY: Nervous system (spinal cord, brain stem,  
CC cerebellum and cerebrum). Not expressed in liver, spleen, kidney,  
CC heart or muscle.  
CC -!- DEVELOPMENTAL STAGE: In cerebral cortex, spinal cord and sciatic  
CC nerve levels are high early in development but decrease during

CC postnatal development and are low in adults. In dorsal root  
 CC ganglia levels remain high throughout development.  
 CC -!- INDUCTION: By nerve growth factor.  
 CC -!- DOMAIN: Has a highly basic region with many copies of the sequence  
 CC KKEE and KKEI/V, repeated but not at fixed intervals, which is  
 CC responsible for the binding of MAP1B to microtubules.  
 CC -!- PTM: LC1 is coexpressed with MAP1B. It is a polypeptide generated  
 CC from MAP1B by proteolytic processing. It is free to associate with  
 CC both MAP1A and MAP1B. It interacts with the amino-terminal region  
 CC of MAP1B (By similarity).  
 CC -!- PTM: Phosphorylated.  
 CC -!- SIMILARITY: TO MAP1A.  
 CC -!- CAUTION: A C-terminal fragment of this protein (residues 1597 to  
 CC 2459) was originally described as neuraxin in Ref.3.

CC -----  
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 CC -----

DR EMBL; U52950; AAB17068.1; -.  
 DR EMBL; X60370; CAC16162.1; -.  
 DR EMBL; X16623; CAA34620.1; ALT\_SEQ.  
 DR PIR; A56577; A56577.  
 DR InterPro; IPR000102; MAP1B\_neuraxin.  
 DR Pfam; PF00414; MAP1B\_neuraxin; 10.  
 DR PROSITE; PS00230; MAP1B\_NEURAXIN; 8.  
 KW Microtubule; Repeat; Phosphorylation.  
 FT CHAIN ? 2459 MAP1 LIGHT CHAIN LC1.  
 FT REPEAT 1869 1885 MAP1B 1.  
 FT REPEAT 1886 1902 MAP1B 2.  
 FT REPEAT 1903 1919 MAP1B 3.  
 FT REPEAT 1920 1936 MAP1B 4.  
 FT REPEAT 1937 1953 MAP1B 5.  
 FT REPEAT 1954 1970 MAP1B 6.  
 FT REPEAT 1988 2004 MAP1B 7.  
 FT REPEAT 2005 2021 MAP1B 8.  
 FT REPEAT 2022 2038 MAP1B 9.  
 FT REPEAT 2039 2055 MAP1B 10.  
 FT DOMAIN 559 1035 GLU-RICH.  
 FT DOMAIN 588 786 LYS-RICH (HIGHLY BASIC, CONTAINS MANY  
 FT KKEE AND KKEI/V REPEATS).  
 FT DOMAIN 2224 2312 LYS-RICH.  
 FT CONFLICT 127 127 M -> V (IN REF. 1).  
 FT CONFLICT 140 140 T -> S (IN REF. 1).  
 FT CONFLICT 2112 2112 R -> K (IN REF. 3).  
 FT CONFLICT 2169 2169 L -> I (IN REF. 3).  
 SQ SEQUENCE 2459 AA; 269497 MW; 2E3F6872DEDB8BA2 CRC64;

Query Match 4.9%; Score 289; DB 1; Length 2459;  
 Best Local Similarity 20.9%; Pred. No. 0.00094;  
 Matches 275; Conservative 158; Mismatches 462; Indels 422; Gaps 61;

Qy 30 EPEDEEEEEEEEEDEDEDLEELEVLERKPAAGLSAAPVPTAPAAGAPLMDFGNDVFPPA 89

Db	1004	EAEQSEEEGEEEEEDKAEDAREEDHEPDKTEAEDYVMAVVDKAAEAGVTEdqY--DFL---	1058
Qy	90	PRGPLPAAPP--VAPERQPSWDPSPVSSTVPAPSPLSAAVSPSKLPEDDEPPARPPPPP	147
Db	1059	---GTPAKQPGVQSPSREPA--SSIHDETLPGGSESEATA-----SDEENREDQPEEF	1106
Qy	148	PASVSPQAEPVWTPPAPAPAAPPSTPAAPKRRGSSGAVVXXXXKIMDLKEQPGNTISAGQ	207
Db	1107	TATSGYTQSTIEISSEPTPMDEMSTP-----RDVMTDETNNREETESPSQ	1150
Qy	208	E-----DFPSVLLETAASXP---SLSPLSAASFKE---HEYLGNLSTVLPTEGTLQENV	255
Db	1151	EFVNITKYESSLYSQEYSKPVVASFENGLSDGSKTDATDGRDYNASASTISPPSSMEEDKF	1210
Qy	256	SEAS-----KEVSEK-----AKTLLIDRDLTE	277
Db	1211	SKSALRDAYRPEETDVKTGAELDIKDVSDERLSPAKSPSLSPSPSPPIEKTPLGERSV-N	1269
Qy	278	FS----ELEYSEMGSFS-VSPKAESAVI---VANPRE---EIIVKNK-----	314
Db	1270	FSLTPNEIKASAEGEATAVSPGVTQAVVEEHCASPEEKTLEVVSQSVTGSAGHTPY	1329
Qy	315	----DEEEKLVSNNILHXQOELPTALTCLKVEDEVVSSE--KAKDSFNEKRVAVEAPMRE	368
Db	1330	QSPTDEKSSHLPTTEVTENAQAVP-----VSFEFTEAKDE-NER--SSISPMDE	1374
Qy	369	EYADFK-PFERVWE-----VKDSKED---SDMLAAGGKIESNLESKVDKKCFADSL	415
Db	1375	PVPDESPIEKVLSPLRSPPLIGSESAYEDFLSADDKALGRRSESPEFGKNGKQGFSD--	1432
Qy	416	EQTNHEKDSSESNDDTSFPSTPEGIKDRSGAYITCAPFNP---AATESIATNIFPLLED-	471
Db	1433	-----KESPVS-DLTSDLYQDKQEEKRAGFIPIKEDFSPEKKASDAEIMSSQSALALDE	1485
Qy	472	-----PTSENXTDEKKIEEKKAQIVTEKNTSTKTSNPFVAAQDSETDYVTTDNLTK	523
Db	1486	RKLGGDGSPTQVDVSQFGSKEDTKMSISEGTVSDKSATPVDEGAEDT---YSHMEGVAS	1542
Qy	524	VTEEVVA--NMPEGLTPDLVQEACESELNEVTGTKIAYETKMDLVQTSEVMQES-LYPAA	580
Db	1543	VSTASVATSSFPPEPTTDD-VSPSLHAEVGSPHSTEVDDSLSVSVVQTPTTFQETEMSPSK	1601
Qy	581	QLCP-----SFESEATPSPVLPDIVMEAPLNSAV-----P	611
Db	1602	EECPRPMISPPDFSPKTAKSRTPVQDHRSEQSSMSIEFGQESPEHSLAMDFSRQSPDHP	1661
Qy	612	SAGASVIQ----PSSSPLEASSVNYESIKHE--PENPPPY-----EEAMSVS-LKVSG	657
Db	1662	TVGAGMLHITENGPTVDYSPSDIQDSSLSHKIPPTTEEPSYTQDNDLSELISVSQVEASP	1721
Qy	658	IKEEIKEPENINAAALQETE-----APYISIACDLIKE---TKLSAEP-----	696
Db	1722	STSSAHTPSQIASPLQEDTLSDVPPRDMSLYASLASEKVQSLEGEKLSPKSDISPLTPR	1781
Qy	697	-----APDFSDYSEMAK-----VEQVPDPHSELVEDS-----	723

Db 1782 ESSPTYSPGFSDSTSGAKESTAAYQTSSSPIDAAAEPYGFRSSMLFDTMQHHLALSRD 1841  
 Qy 724 -----SPDSEPVDLFSDD---SIPDVP---QKQD 746  
 ||| | | | : || :  
 Db 1842 LTTSSVEKDNGGKTPGDFNYAYQKPESTTESPDEEDYDYESHEKTIQAHDVGGYYYEkte 1901  
 Qy 747 ETVML-----VKESLTETSFESMIEYENKEKLSALPPEGGKPYLESFKLSLDNTKD 797  
 |: | |:| : | || : ||| | : :  
 Db 1902 RTIKSPCDSGYSYETIEKTTKTPEDGGYSCEITEKTTTRTPEEGGYSY-----EISEK 1953  
 Qy 798 TLLPDEVs--TLskKEKIPLQMEELSTAVYSNDD-----LFISKEA 836  
 | ||| | | |: :::| :| | | :  
 Db 1954 TTRTPEVSGYTYEKTERRRLDDISNGYDDTEDGGHTLGDCSYSYETTEKITSFPESES 2013  
 Qy 837 QIRETETFSdSSP-----IEIIDEFPTLISSKTDSFSKLAREYT-----DL 877  
 || | : || | ::: : | | : || |  
 Db 2014 YSYETTTKTTSPDTSAYCYETMEKITKTPQASTYSYETSDRCYTPERKSPSEARQDVDL 2073  
 Qy 878 -----EVSH-KSEIANA---PDG---AGSLPCTELPHDLsLKNIQP-----KV 913  
 | | |:|:: : |: || | | : | :  
 Db 2074 CLVSSCEFKHPKTELSPSFINPNLEWFAGEEPTESERPLTQSGGAPPPSGGKQQRQC 2133  
 Qy 914 EEKISFSDDFSKNGSATSkvLLLLPPDVsalGHTQAEIESIVKPKVLEKEAEKK-LPSD-- 970  
 :| | | | | ||: | || |: | | : :|:|  
 Db 2134 DETPPTSVSESAPSQTDSdV---PPETE-----ECPSITADANLDSEDESEtiPTDKT 2183  
 Qy 971 -----TEKEDRSPS-----AIFSADLGKTSVVDLLYWRDIKKTG 1004  
 :|||| | :|| | | |  
 Db 2184 VTYKHMDPPPAPMQDRSPSPRHPDVSMVDPEALAIEQNLGKALKKDLKEKAKTKKPG 2240

Search completed: September 29, 2004, 18:14:46  
 Job time : 24.8874 secs